Express Mail Label No. EV132183890US

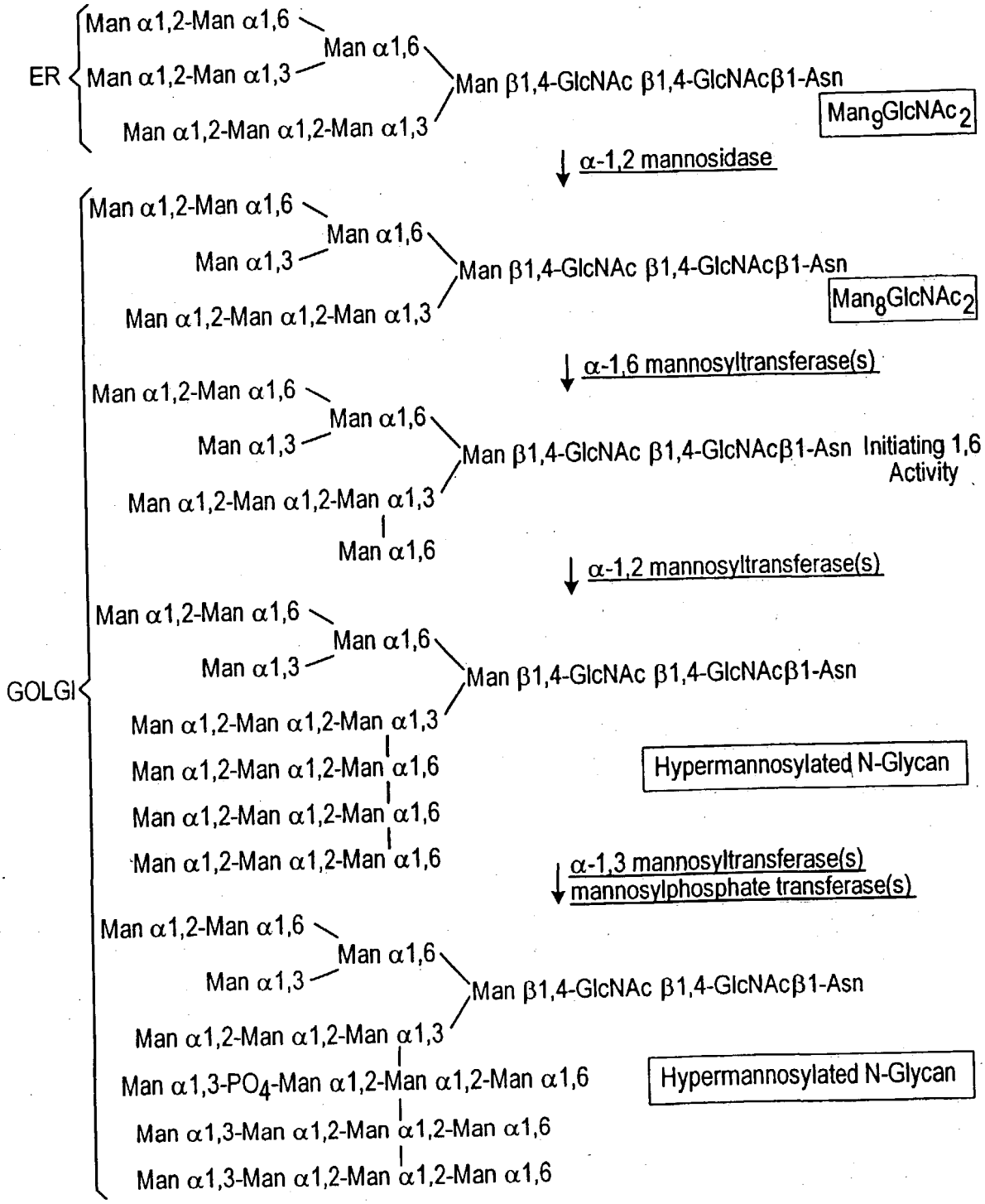


FIG. 1A

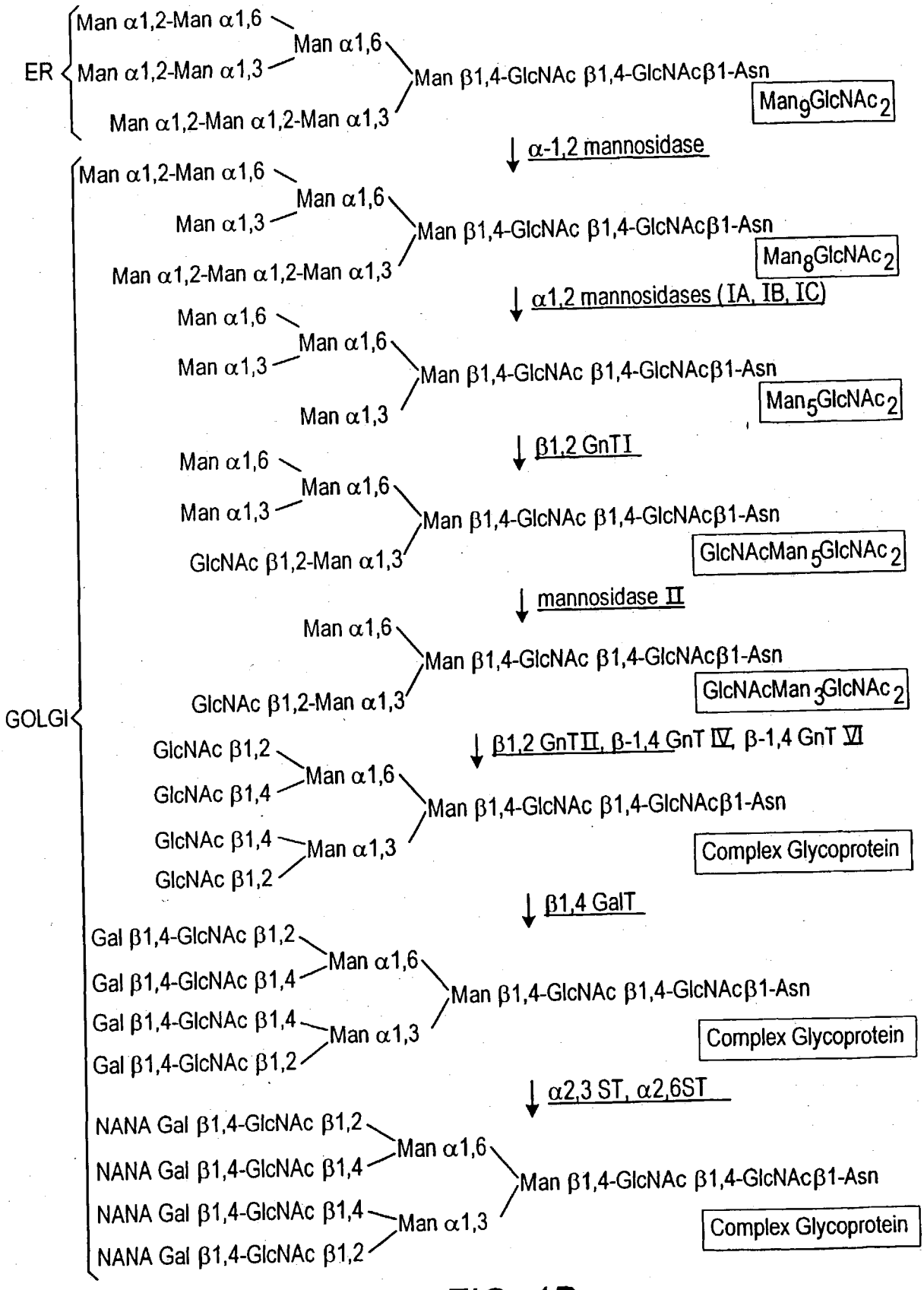

ER
Man α1,2-Man α1,6
Man α1,6
Man α1,2-Man α1,3
Man α1,2-Man α1,2-Man α1,3
Man β1,4-GlcNAc β1,4-GlcNAcβ1-Asn
Man9GlcNAc2
α-1,2 mannosidase
Man8GlcNAc2
α1,2 mannosidases (IA, IB, IC)
Man5GlcNAc2
β1,2 GnTI
GlcNAcMan5GlcNAc2
mannosidase II
GlcNAcMan3GlcNAc2
β1,2 GnTII, β-1,4 GnT IV, β-1,4 GnT VI
GlcNAc β1,2
GlcNAc β1,4
Man α1,3
Complex Glycoprotein
β1,4 GalT
Gal β1,4-GlcNAc β1,2
Gal β1,4-GlcNAc β1,4
α2,3 ST, α2,6ST
NANA Gal β1,4-GlcNAc β1,2
NANA Gal β1,4-GlcNAc β1,4
GOLGI

FIG. 1B

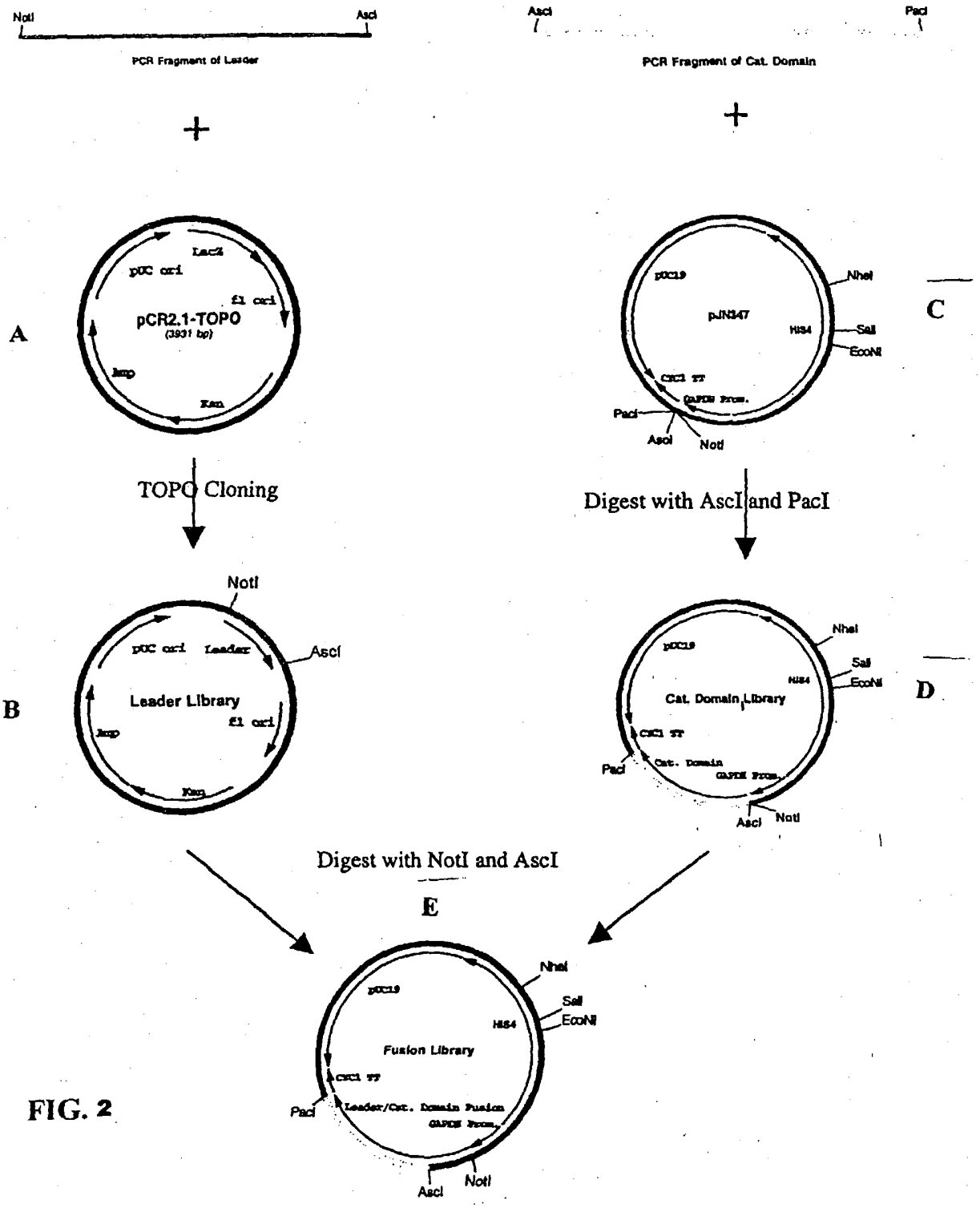
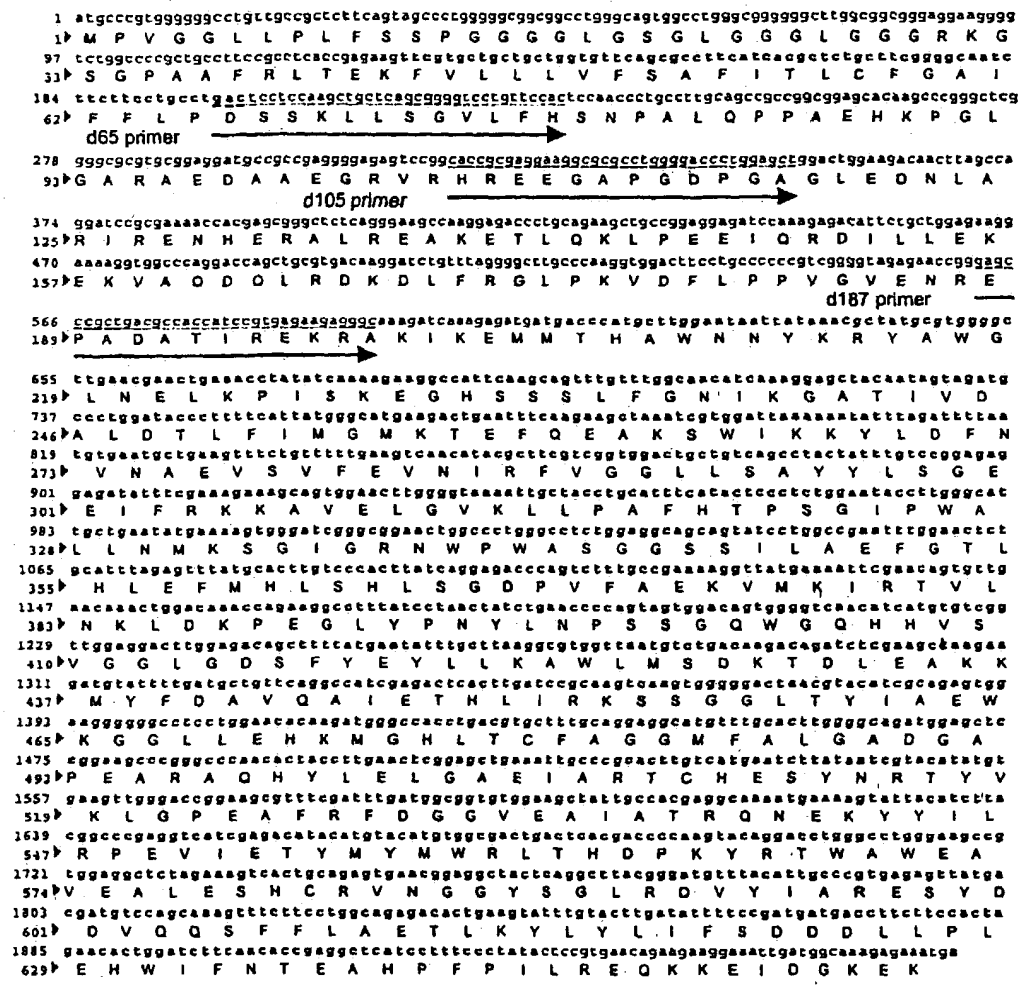

NotI
AscI
PCR Fragment of Leader
+
AscI
PacI
PCR Fragment of Cat. Domain
+
A
pUC ori
LacZ
f1 ori
pCR2.1-TOPO
(3931 bp)
Amp
Kan
TOPO Cloning
B
NotI
pUC ori
Leader
AscI
Leader Library
f1 ori
Amp
Kan
C
pUC19
NheI
pJN347
HIS4
SalI
EcoNI
CYC1 TT
GAPDH Prom.
PacI
AscI
NotI
Digest with AscI and PacI
D
pUC19
NheI
SalI
HIS4
EcoNI
Cat. Domain Library
CYC1 TT
PacI
Cat. Domain
GAPDH Prom.
AscI
NotI
Digest with NotI and AscI
E
pUC19
NheI
SalI
HIS4
EcoNI
Fusion Library
CYC1 TT
PacI
Leader/Cat. Domain Fusion
GAPDH Prom.
AscI
NotI

FIG. 2

FIG. 3

M. musculus alpha-1,2-mannosidase IA open reading frame. The transmembrane and catalytic domains are highlighted in bold respectively. The sequence of the primers used to generate the N-terminal truncations are highlighted by underlining and the start of each respective protein fragment indicated by an arrow.



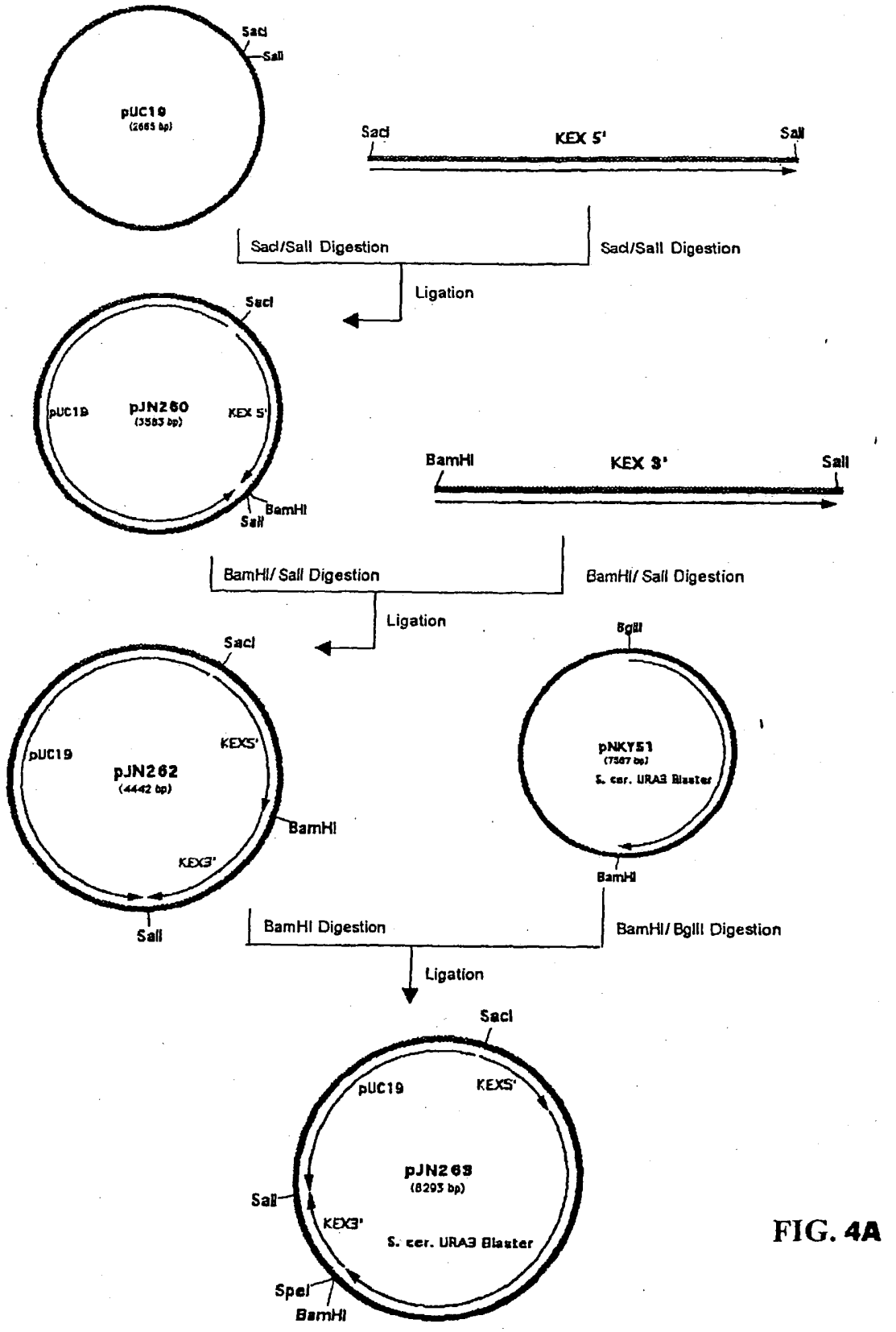

SacI
SalI
pUC19
(2665 bp)
SacI
KEX 5'
SalI
SacI/SalI Digestion
SacI/SalI Digestion
Ligation
SacI
pUC19
pJN260
(3583 bp)
KEX 5'
BamHI
SalI
BamHI
KEX 3'
SalI
BamHI/ SalI Digestion
BamHI/ SalI Digestion
Ligation
SacI
pUC19
KEX5'
pJN262
(4442 bp)
BamHI
KEX3'
SalI
BglII
pNKY51
(7367 bp)
S. cer. URA3 Blaster
BamHI
BamHI Digestion
BamHI/ BglII Digestion
Ligation
SacI
pUC19
KEX5'
pJN263
(8293 bp)
SalI
KEX3'
S. cer. URA3 Blaster
SpeI
BamHI

FIG. 4A

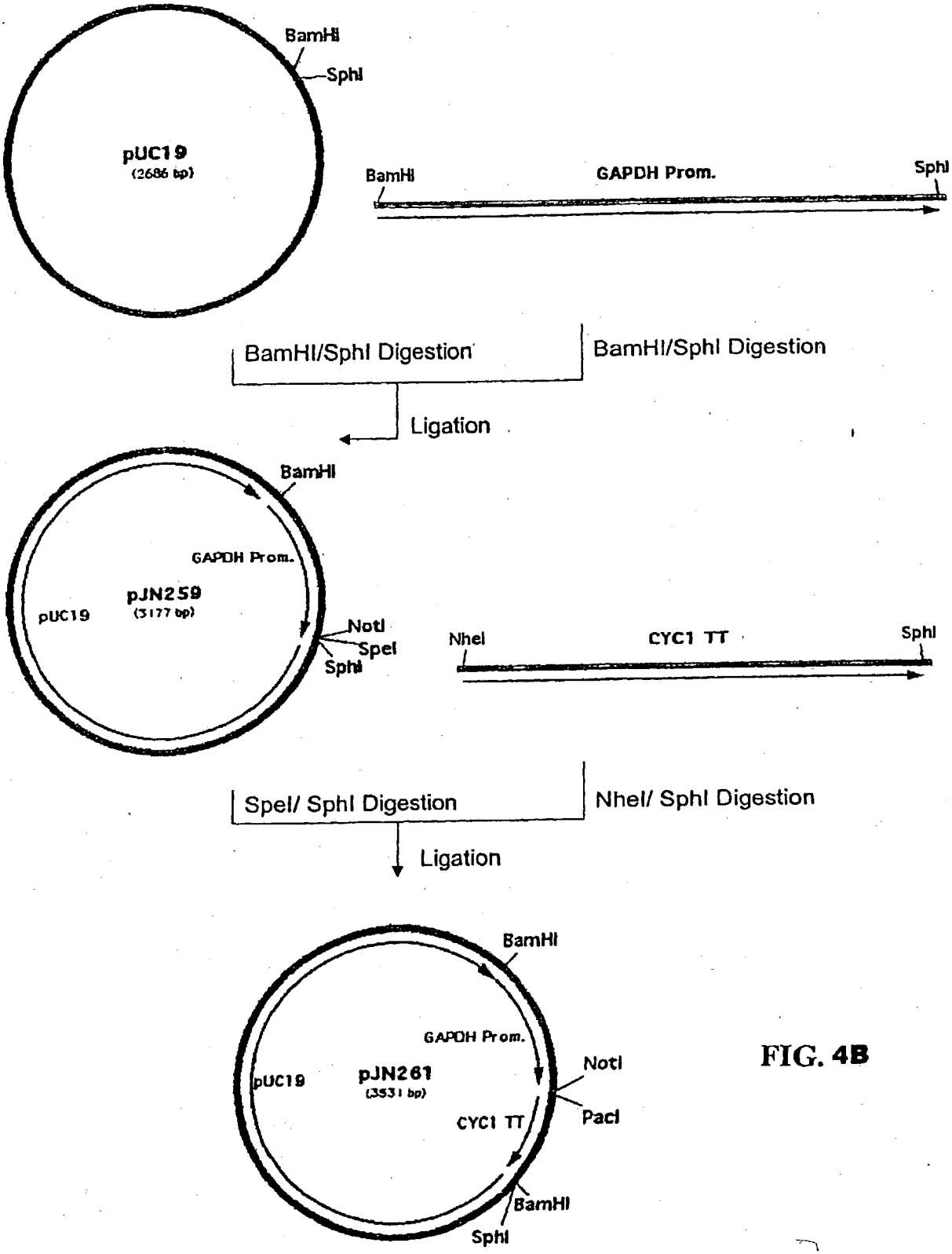

BamHI
SphI
pUC19
(2686 bp)
BamHI
GAPDH Prom.
SphI
BamHI/SphI Digestion
BamHI/SphI Digestion
Ligation
BamHI
GAPDH Prom.
pJN259
(3177 bp)
pUC19
NotI
SpeI
SphI
NheI
CYC1 TT
SphI
SpeI/ SphI Digestion
NheI/ SphI Digestion
Ligation
BamHI
GAPDH Prom.
pJN261
(3531 bp)
pUC19
NotI
PacI
CYC1 TT
BamHI
SphI

FIG. 4B

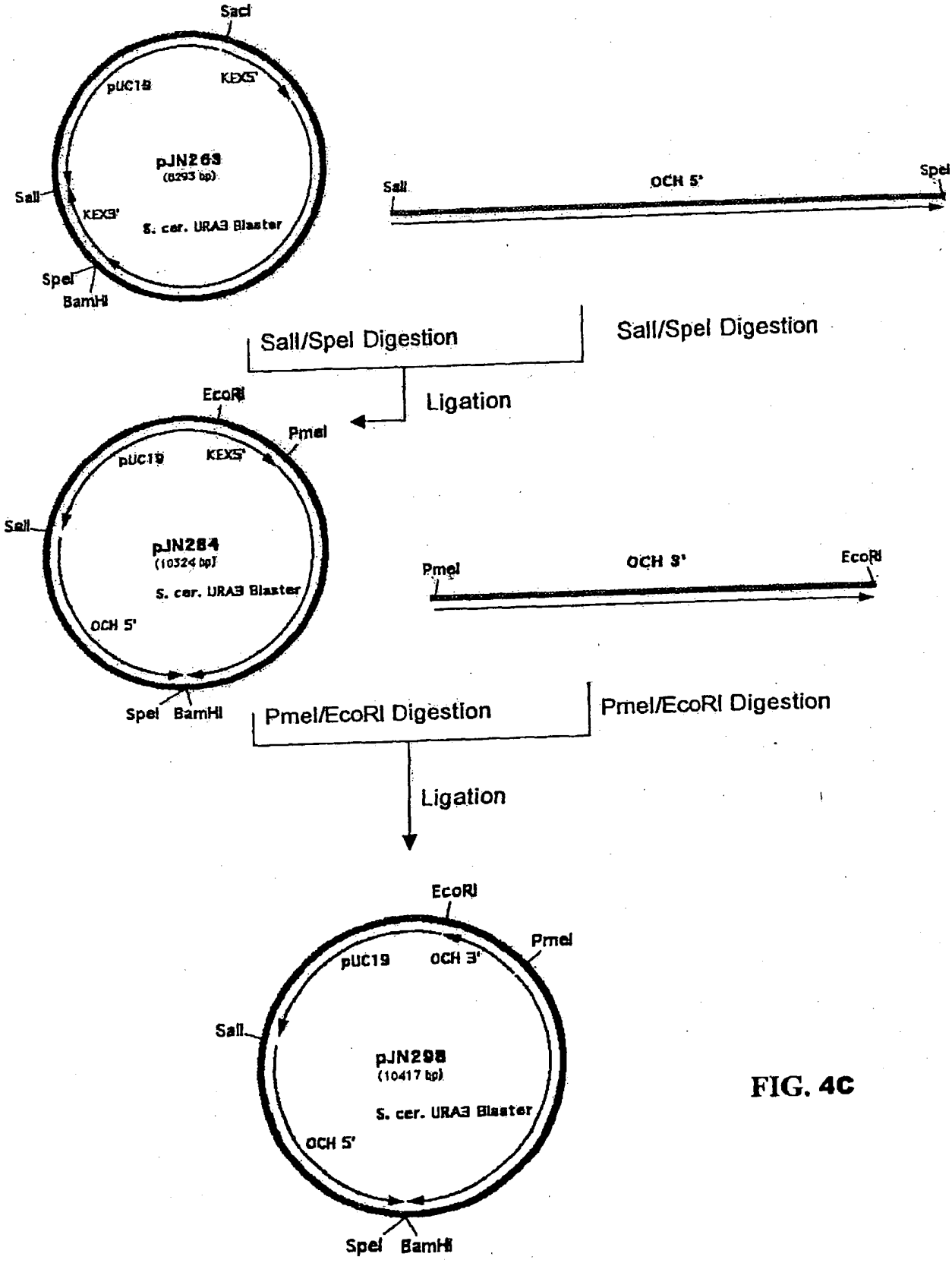

SacI
pUC19
KEX5'
pJN263
(8293 bp)
SalI
KEX3'
S. cer. URA3 Blaster
SpeI
BamHI
SalI
OCH 5'
SpeI
SalI/SpeI Digestion
SalI/SpeI Digestion
Ligation
EcoRI
PmeI
pUC19
KEX5'
SalI
pJN284
(10324 bp)
S. cer. URA3 Blaster
OCH 5'
SpeI
BamHI
PmeI
OCH 3'
EcoRI
PmeI/EcoRI Digestion
PmeI/EcoRI Digestion
Ligation
EcoRI
PmeI
pUC19
OCH 3'
SalI
pJN298
(10417 bp)
S. cer. URA3 Blaster
OCH 5'
SpeI
BamHI

FIG. 4C

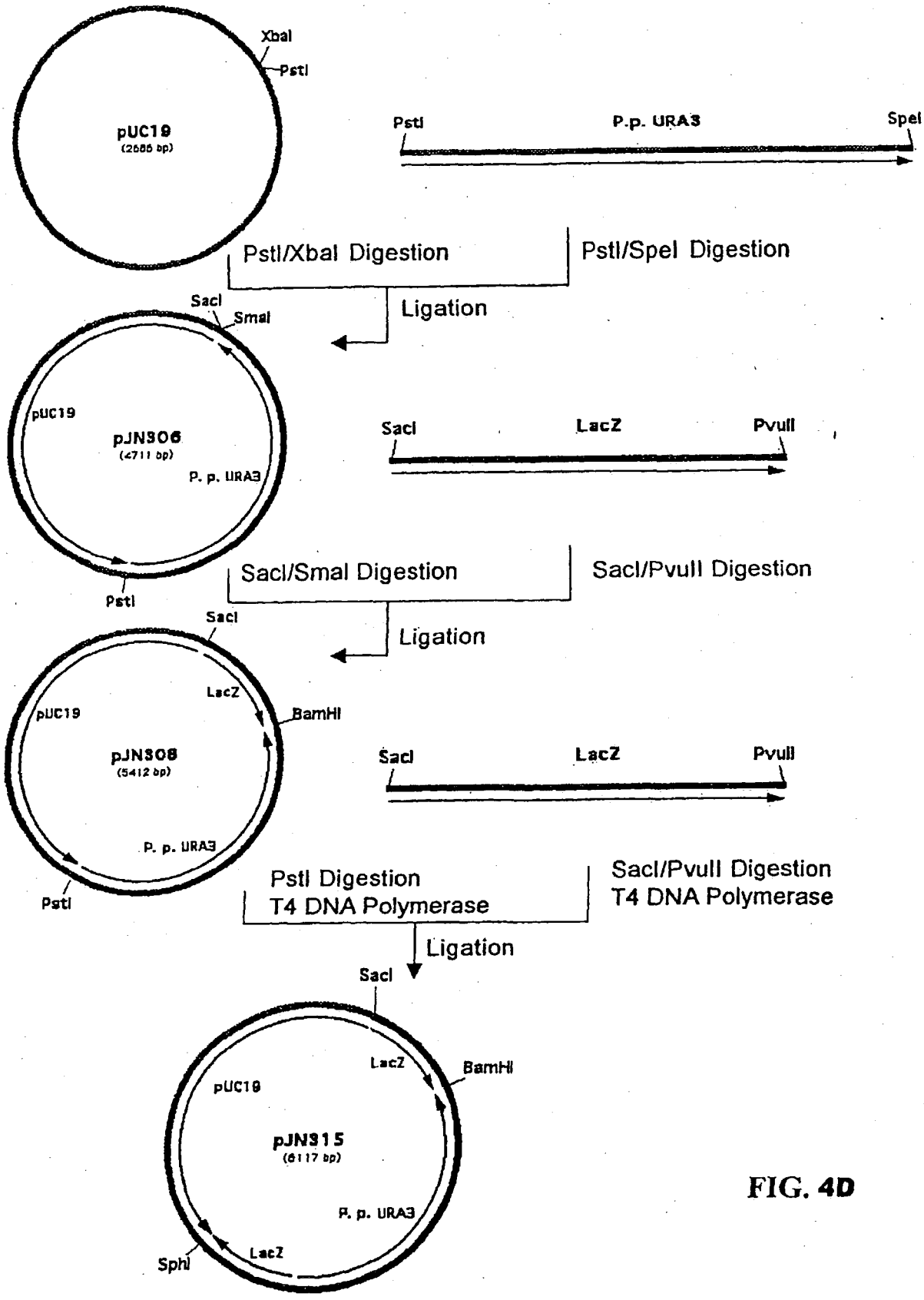

XbaI
PstI
pUC19
(2686 bp)
PstI
P.p. URA3
SpeI
PstI/XbaI Digestion
PstI/SpeI Digestion
Ligation
SacI
SmaI
pUC19
pJN306
(4711 bp)
P. p. URA3
PstI
SacI
LacZ
PvuII
SacI/SmaI Digestion
SacI/PvuII Digestion
Ligation
SacI
LacZ
pUC19
BamHI
pJN308
(5412 bp)
P. p. URA3
PstI
SacI
LacZ
PvuII
PstI Digestion
T4 DNA Polymerase
SacI/PvuII Digestion
T4 DNA Polymerase
Ligation
SacI
LacZ
BamHI
pUC19
pJN315
(6117 bp)
P. p. URA3
SphI
LacZ

FIG. 4D

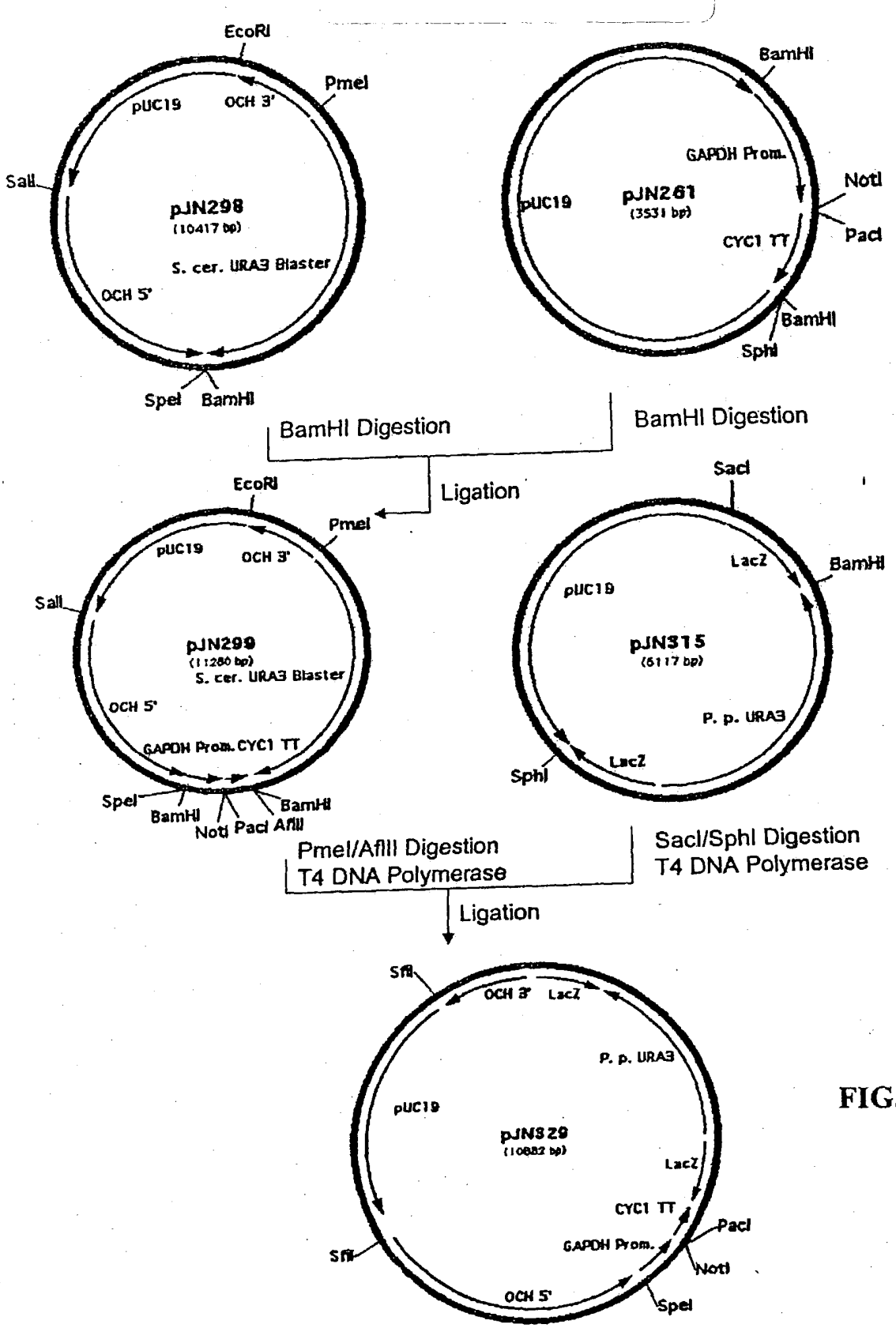

EcoRI
PmeI
pUC19
OCH 3'
SalI
pJN298
(10417 bp)
S. cer. URA3 Blaster
OCH 5'
SpeI
BamHI
BamHI
GAPDH Prom.
NotI
pUC19
pJN261
(3531 bp)
CYC1 TT
PacI
BamHI
SphI
BamHI Digestion
BamHI Digestion
Ligation
EcoRI
PmeI
pUC19
OCH 3'
SalI
pJN299
(11280 bp)
S. cer. URA3 Blaster
OCH 5'
GAPDH Prom.
CYC1 TT
SpeI
BamHI
BamHI
NotI
PacI
AflII
SacI
LacZ
BamHI
pUC19
pJN315
(6117 bp)
P. p. URA3
LacZ
SphI
PmeI/AflII Digestion
T4 DNA Polymerase
SacI/SphI Digestion
T4 DNA Polymerase
Ligation
SfiI
OCH 3'
LacZ
P. p. URA3
pUC19
pJN329
(10882 bp)
LacZ
CYC1 TT
PacI
GAPDH Prom.
NotI
SfiI
OCH 5'
SpeI

FIG. 4E

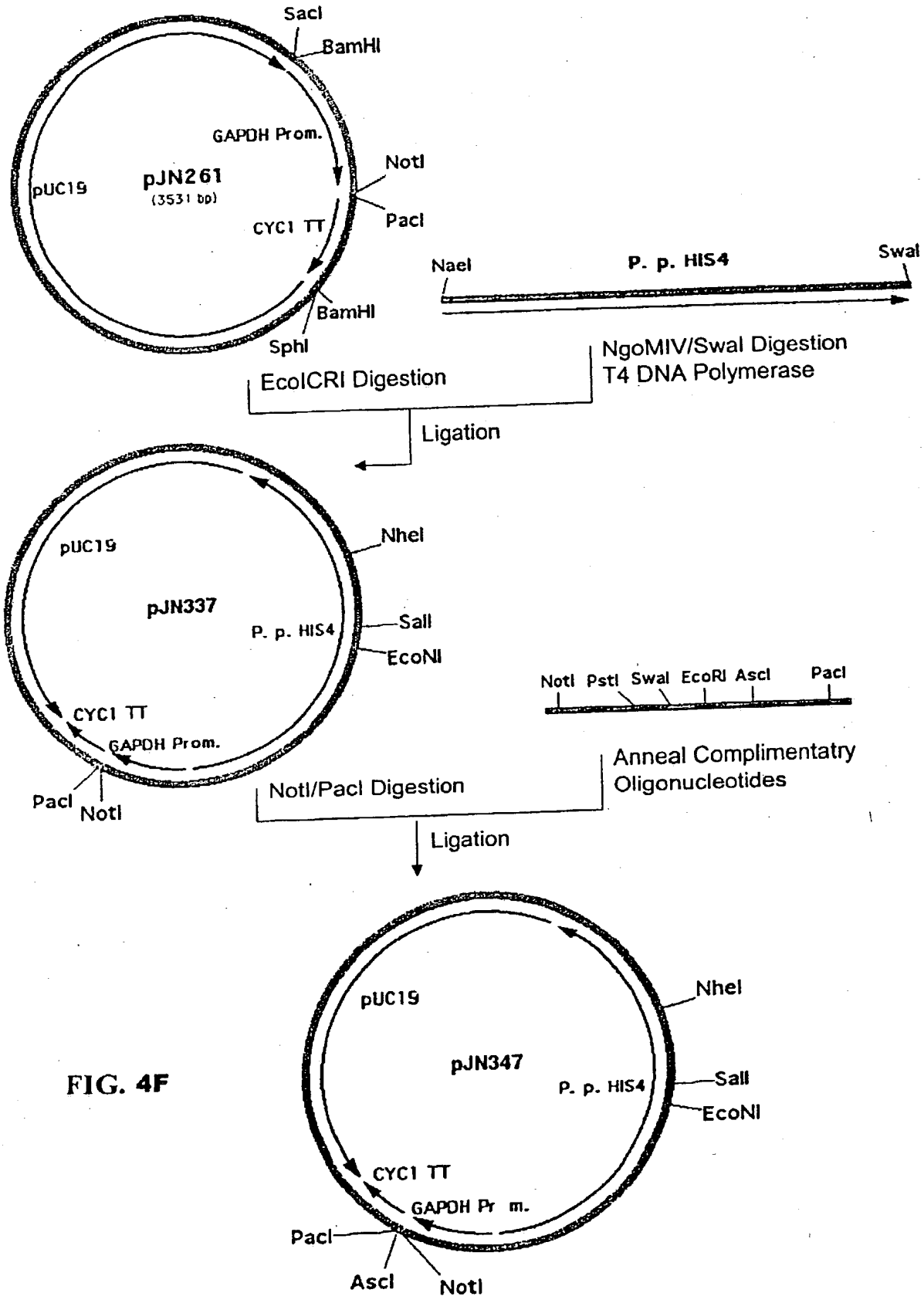

SacI
BamHI
GAPDH Prom.
pJN261
(3531 bp)
pUC19
NotI
PacI
CYC1 TT
BamHI
SphI
NaeI
P. p. HIS4
SwaI
NgoMIV/SwaI Digestion
T4 DNA Polymerase
EcoICRI Digestion
Ligation
pUC19
pJN337
NheI
SalI
P. p. HIS4
EcoNI
CYC1 TT
GAPDH Prom.
PacI
NotI
NotI PstI SwaI EcoRI AscI PacI
Anneal Complimentatry Oligonucleotides
NotI/PacI Digestion
Ligation
pUC19
pJN347
NheI
SalI
P. p. HIS4
EcoNI
CYC1 TT
GAPDH Pr m.
PacI
AscI
NotI

FIG. 4F

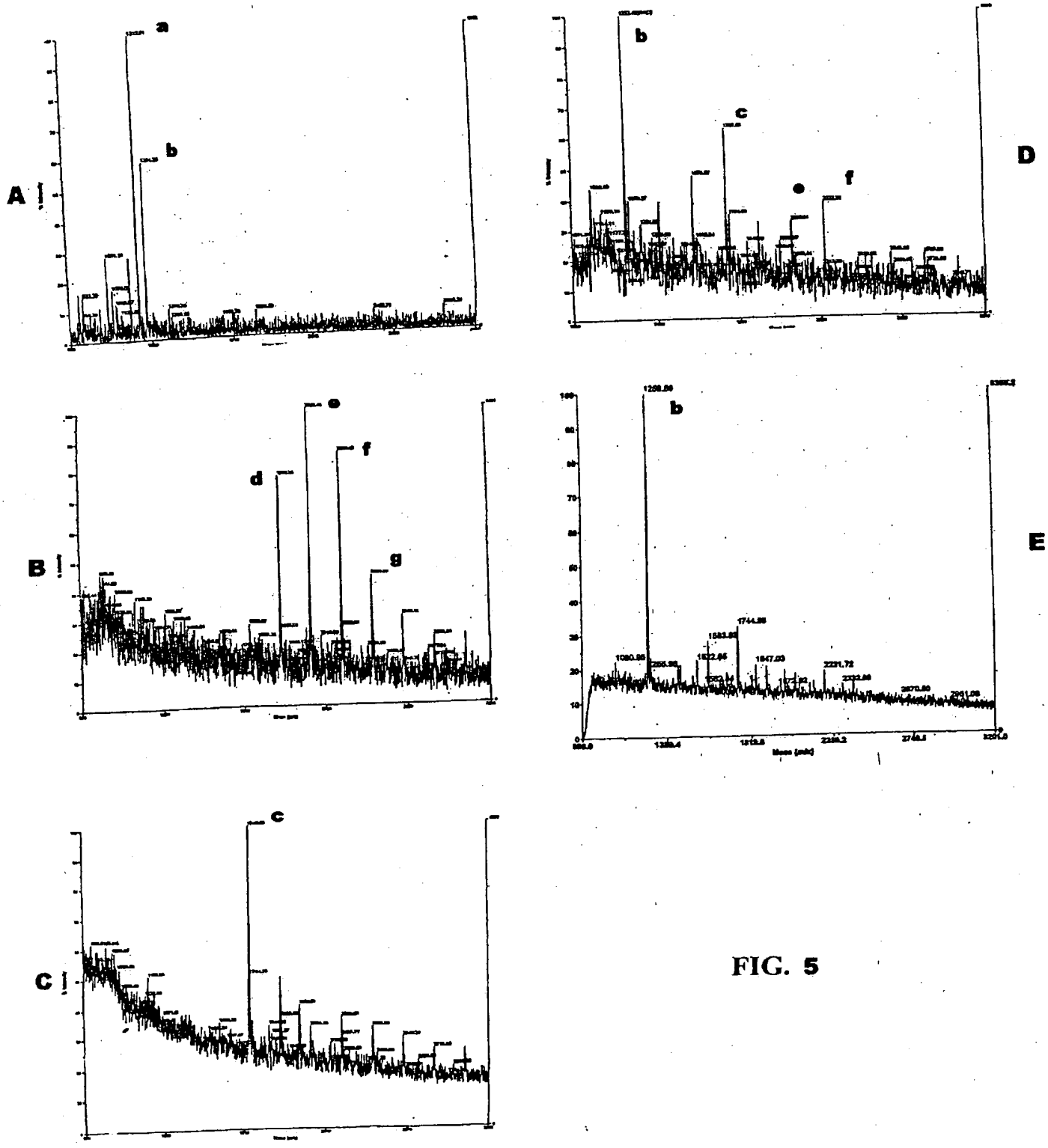
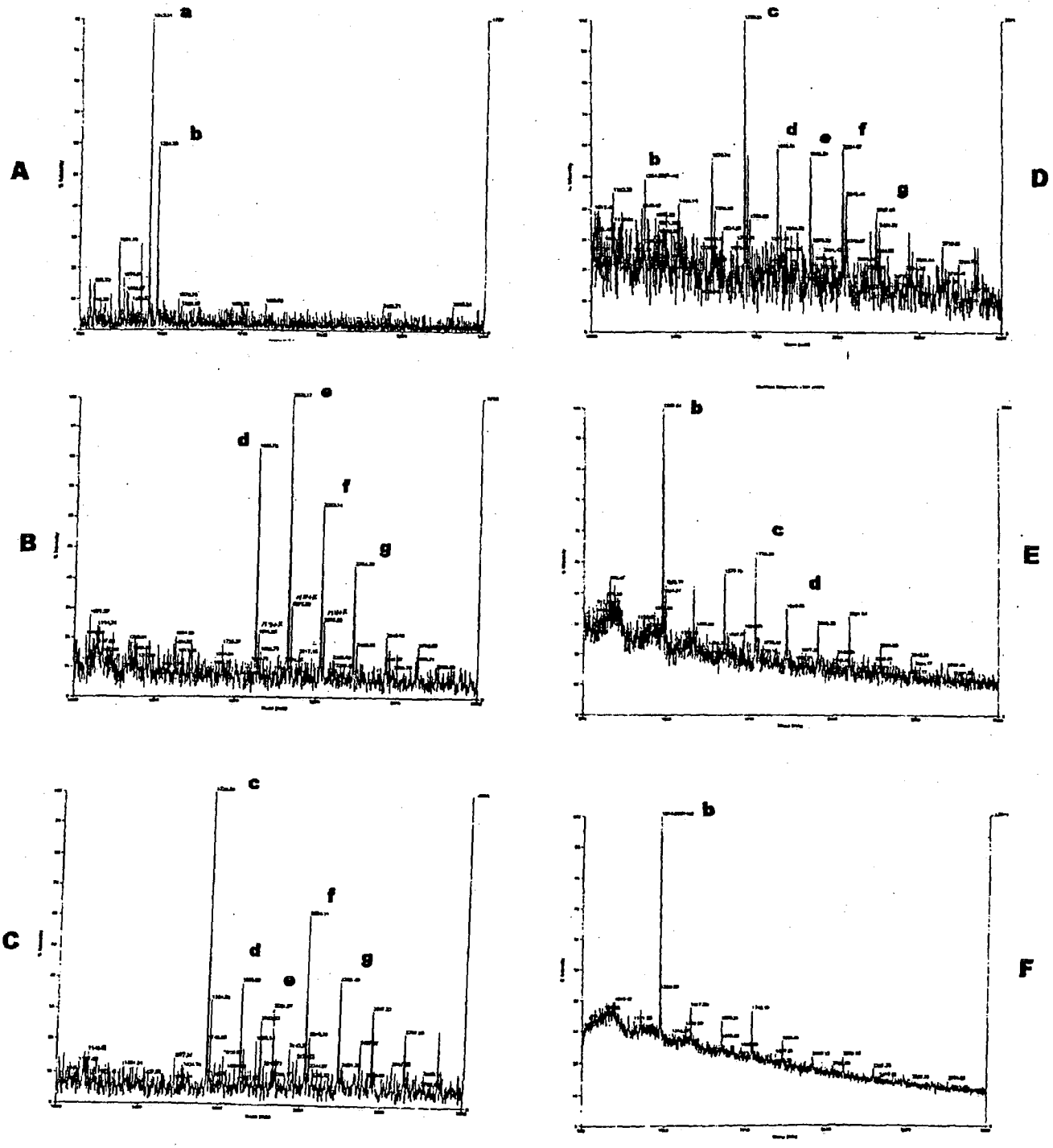
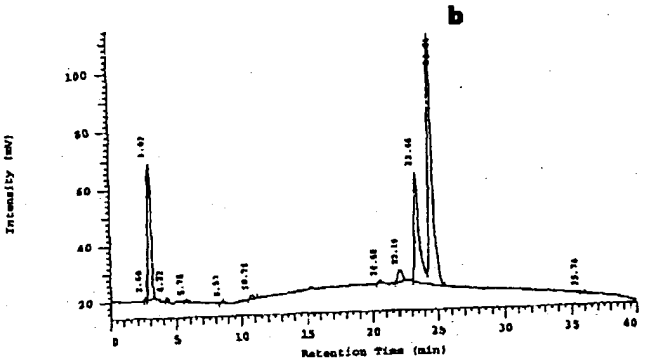

A
a
b
B
d
e
f
g
C
c
D
b
c
e
f
E
b
1744.88
1583.86
1632.86
1080.86
1847.03
2231.72
2333.88
2670.80
2951.08

FIG. 5

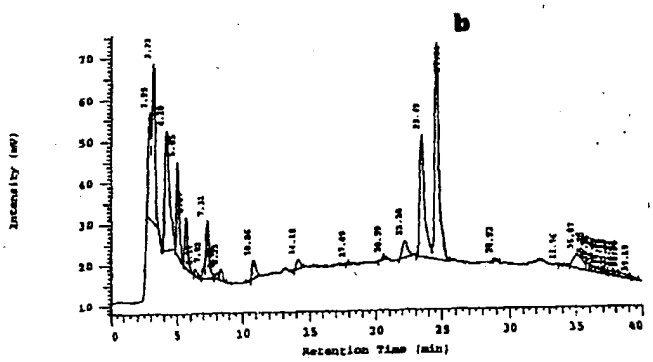
FIG. 6



A


b
Intensity (mV)
Retention Time (min)

B


b
Intensity (mV)
Retention Time (min)

C

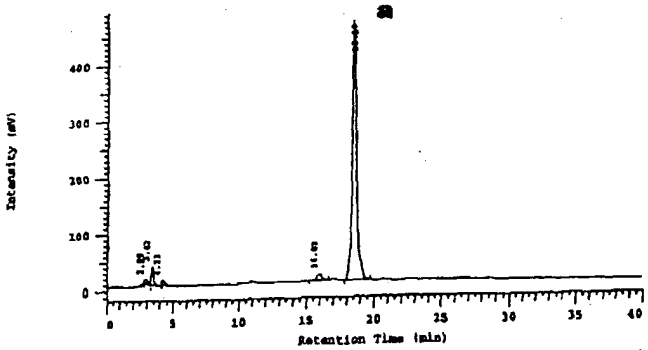
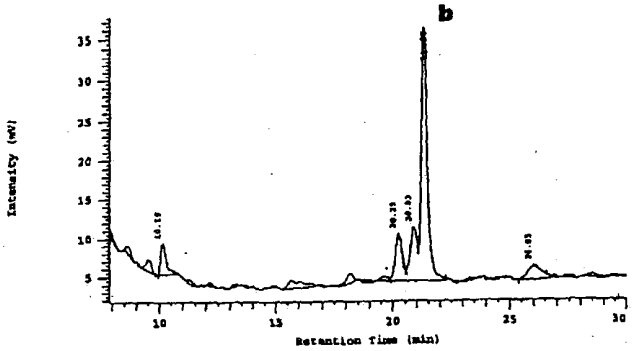
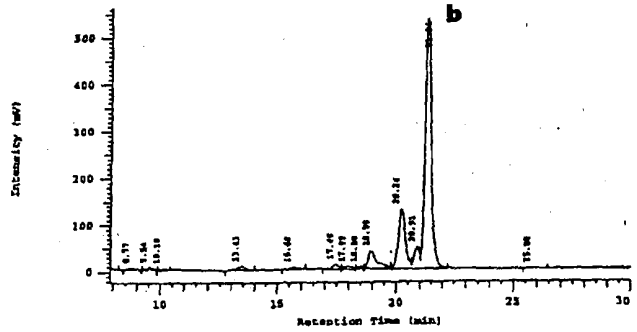

a
Intensity (mV)
Retention Time (min)

FIG. 7

A


b
Intensity (mV)
Retention Time (min)

B


b
Intensity (mV)
Retention Time (min)

C

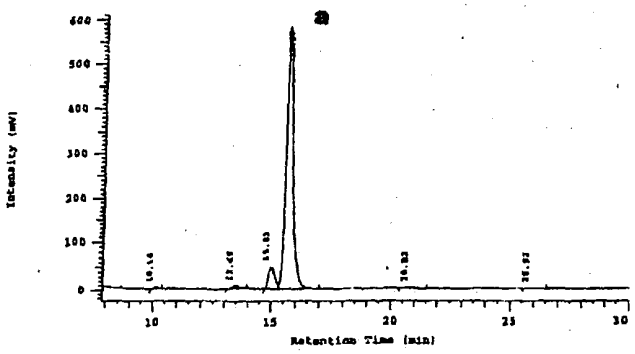
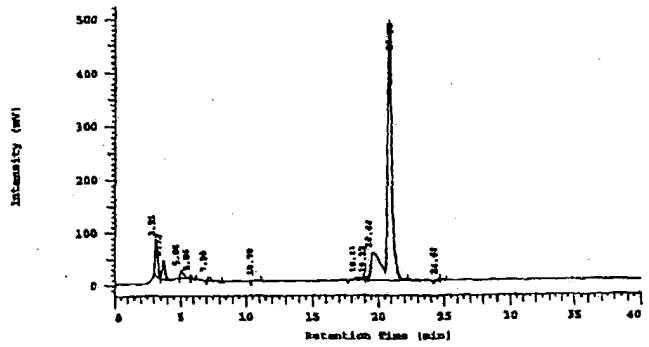
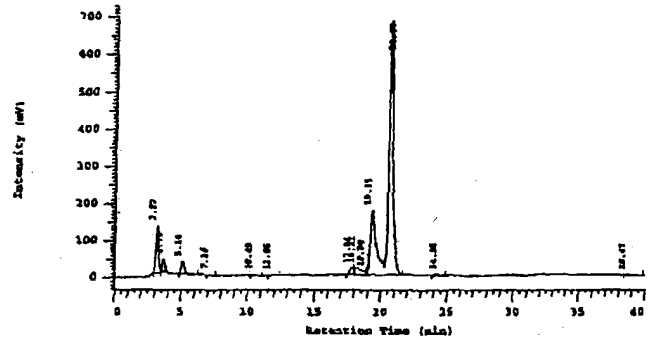

a
Intensity (mV)
Retention Time (min)

FIG. 8

A


Intensity (mV)
Retention Time (min)

B


Intensity (mV)
Retention Time (min)

C

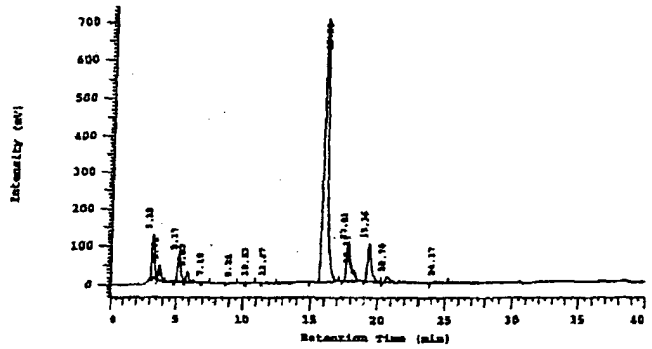
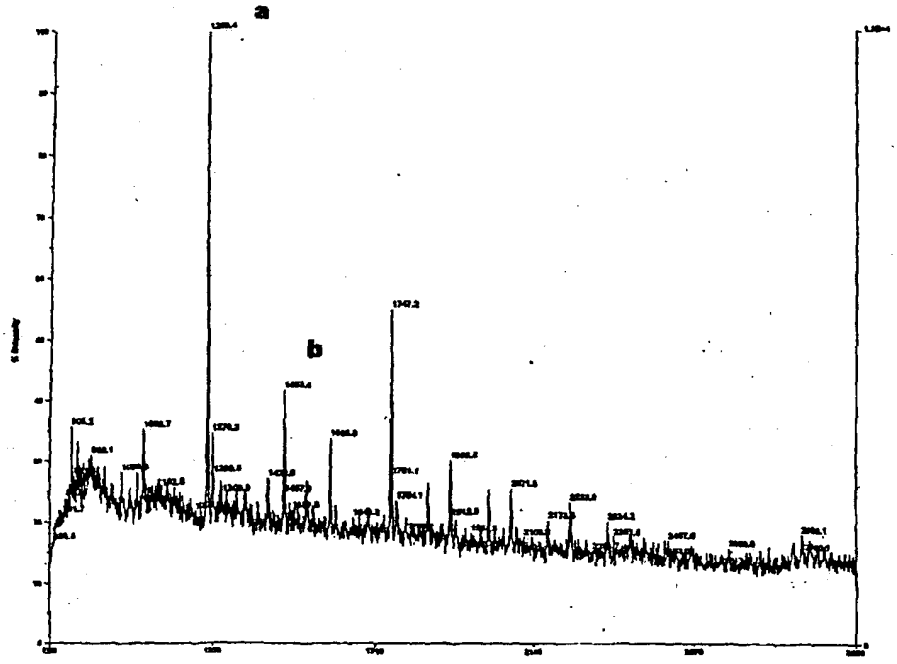
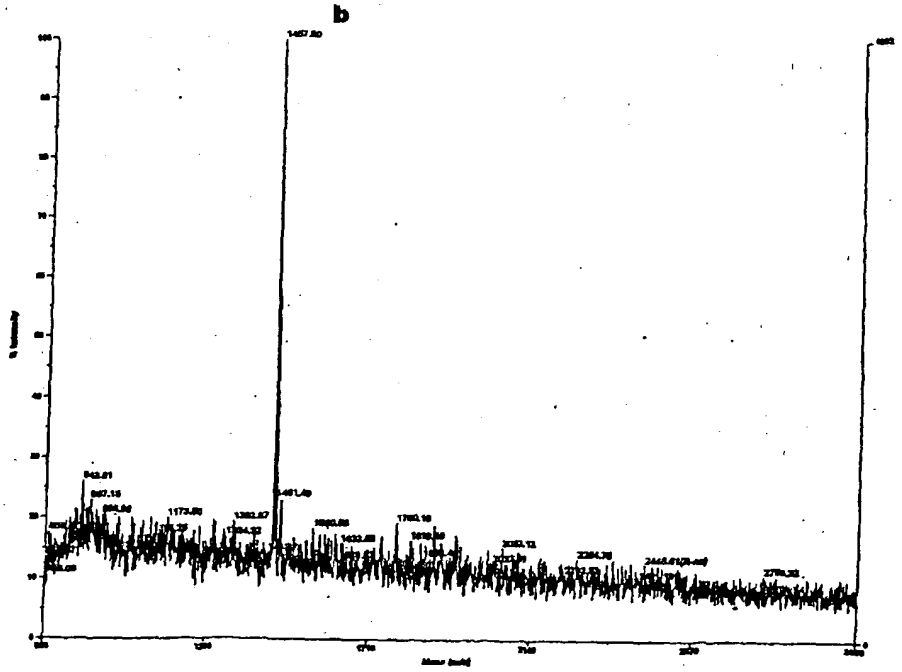

Intensity (mV)
Retention Time (min)

FIG. 9

FIG. 10



A



B

pH optimum f r BB27-2 medium
C. elegans Mann1B D31 and S. Mnn10-s

pH	% of Man5
4.5	0
5	32
5.5	41
6	35
6.43	22
6.5	4
7.5	0
8.5	0

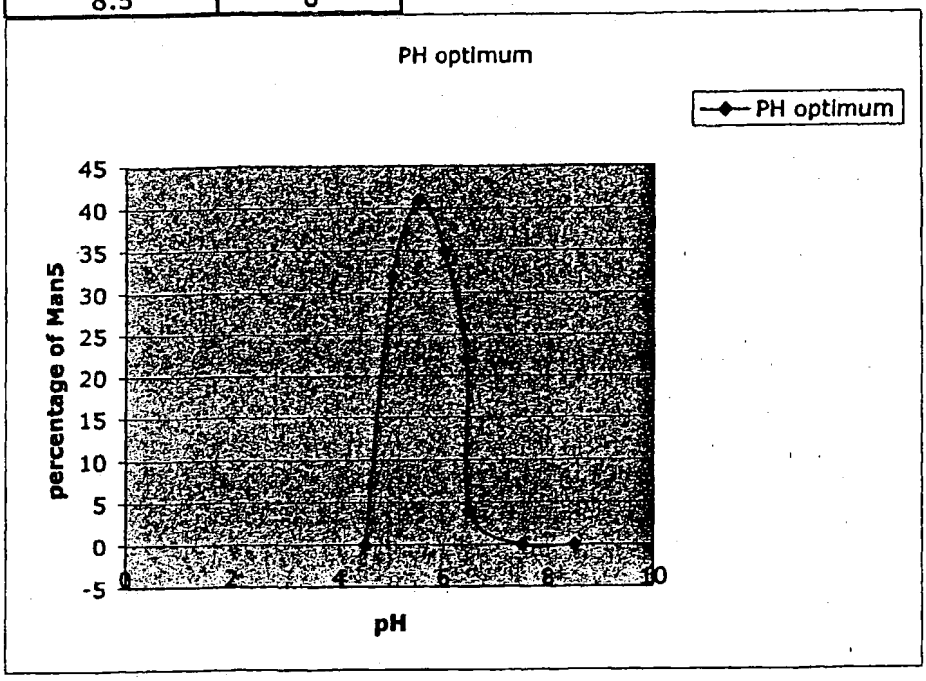
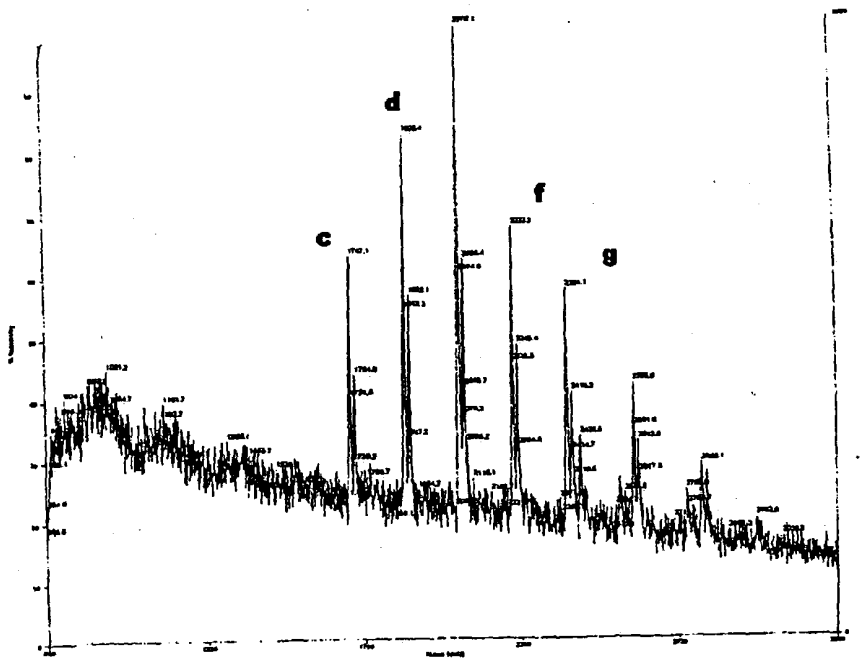
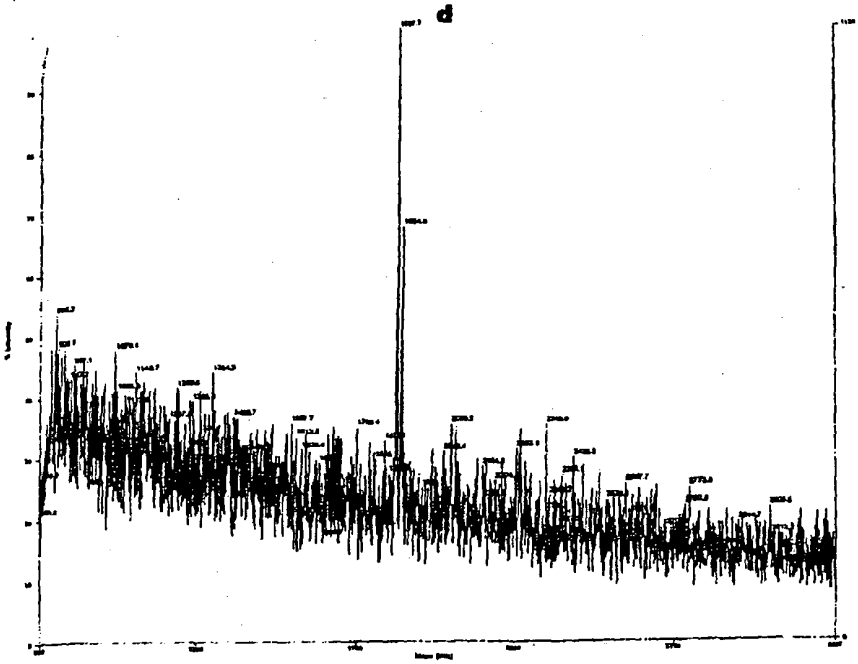


FIG. 11



A

FIG. 12



B

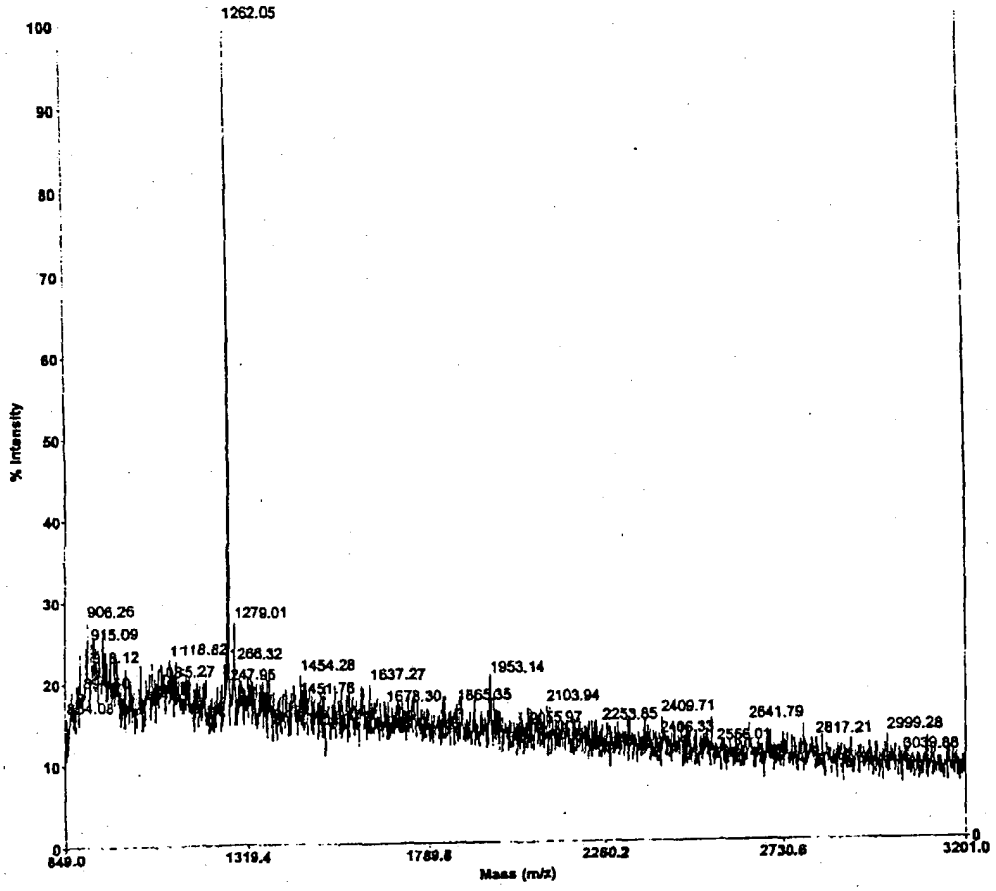

1262.05
100
90
80
70
60
50
40
30
20
10
0
% Intensity
906.26
915.09
1279.01
1118.62
1266.32
1454.28
1637.27
1953.14
2103.94
2409.71
2641.79
2817.21
2999.28
849.0
1319.4
1789.8
2260.2
2730.6
3201.0
Mass (m/z)

FIG. 12C

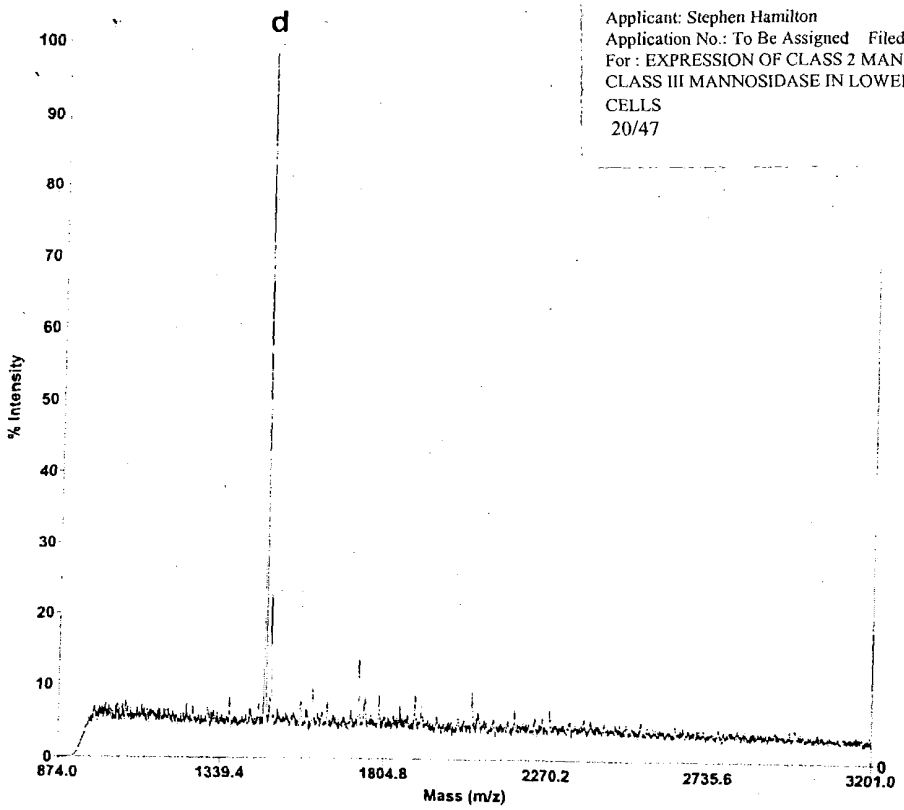

d
100
90
80
70
60
50
40
30
20
10
0
% Intensity
874.0
1339.4
1804.8
2270.2
2735.6
3201.0
Mass (m/z)

FIG. 13

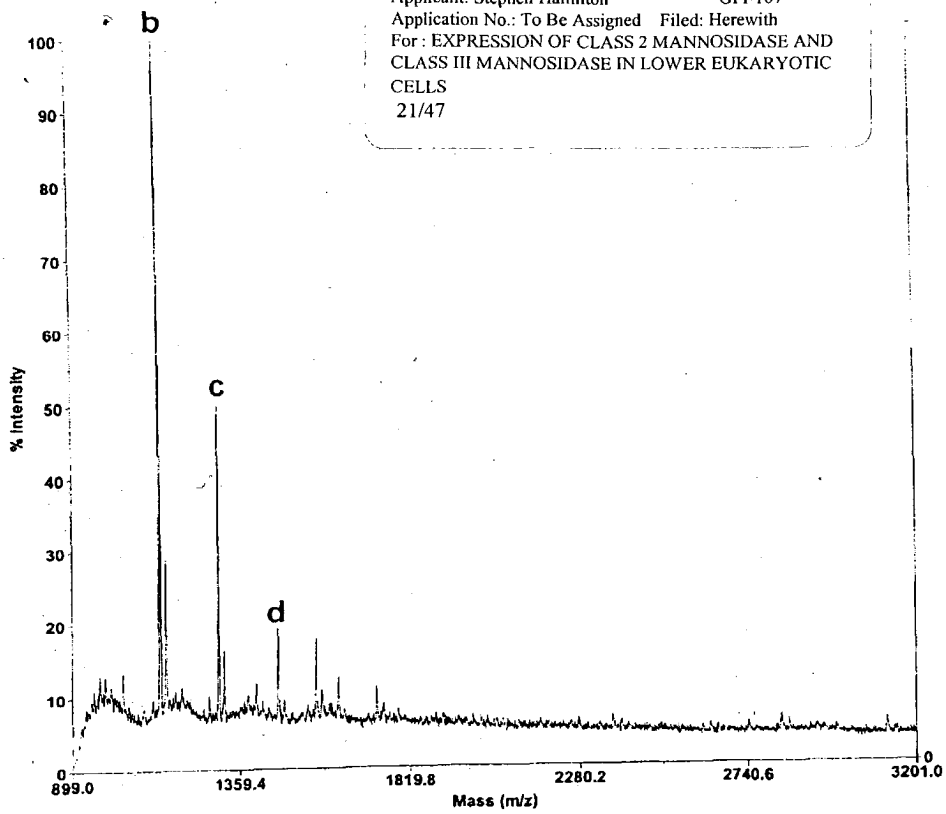

b
c
d
100
90
80
70
60
50
40
30
20
10
0
% Intensity
899.0
1359.4
1819.8
2280.2
2740.6
3201.0
Mass (m/z)

FIG. 14

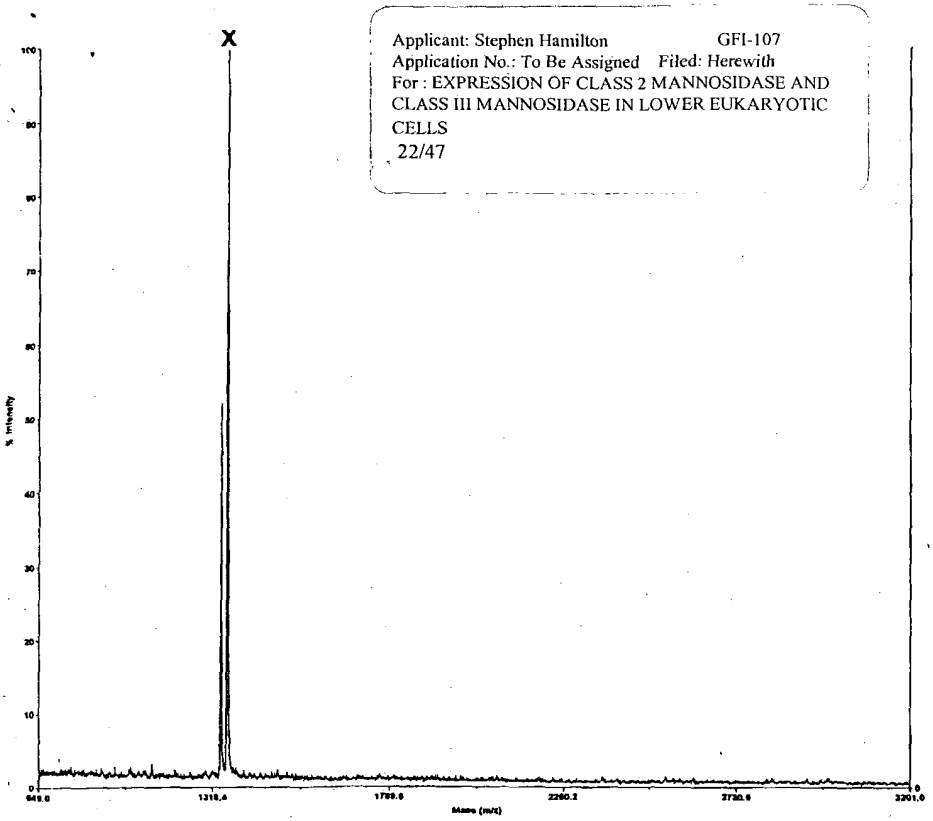

X
% Intensity
100
90
80
70
60
50
40
30
20
10
0
1318.4
2260.2
3201.0
Mass (m/z)

FIG. 15

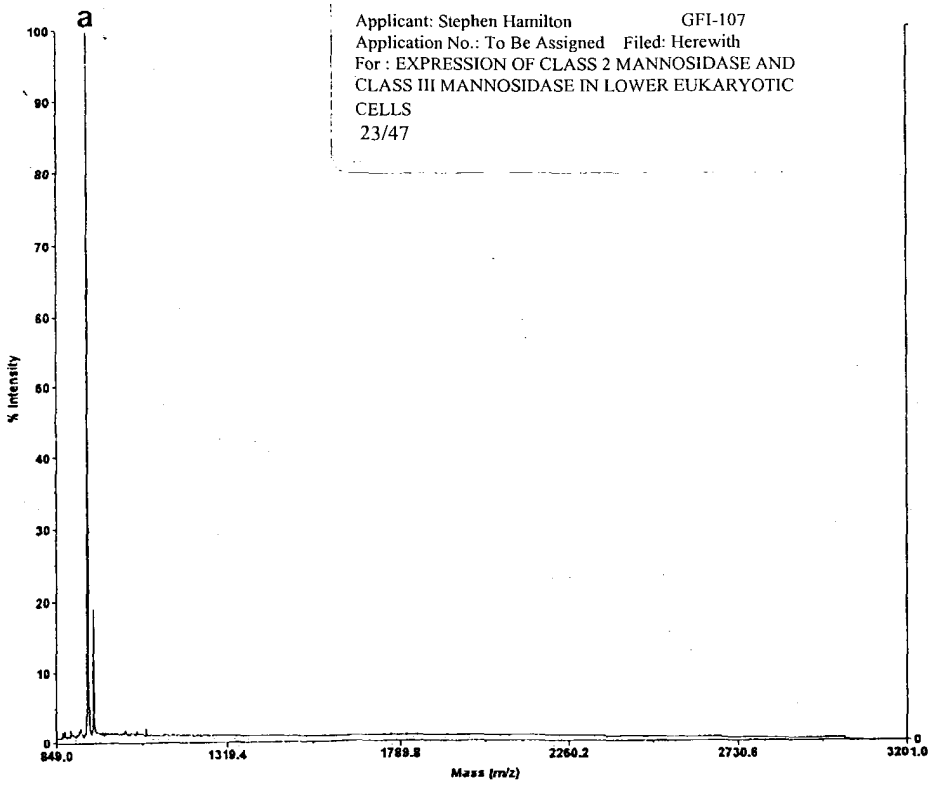

a
% Intensity
100
90
80
70
60
50
40
30
20
10
0
849.0
1319.4
1789.8
2260.2
2730.6
3201.0
Mass (m/z)

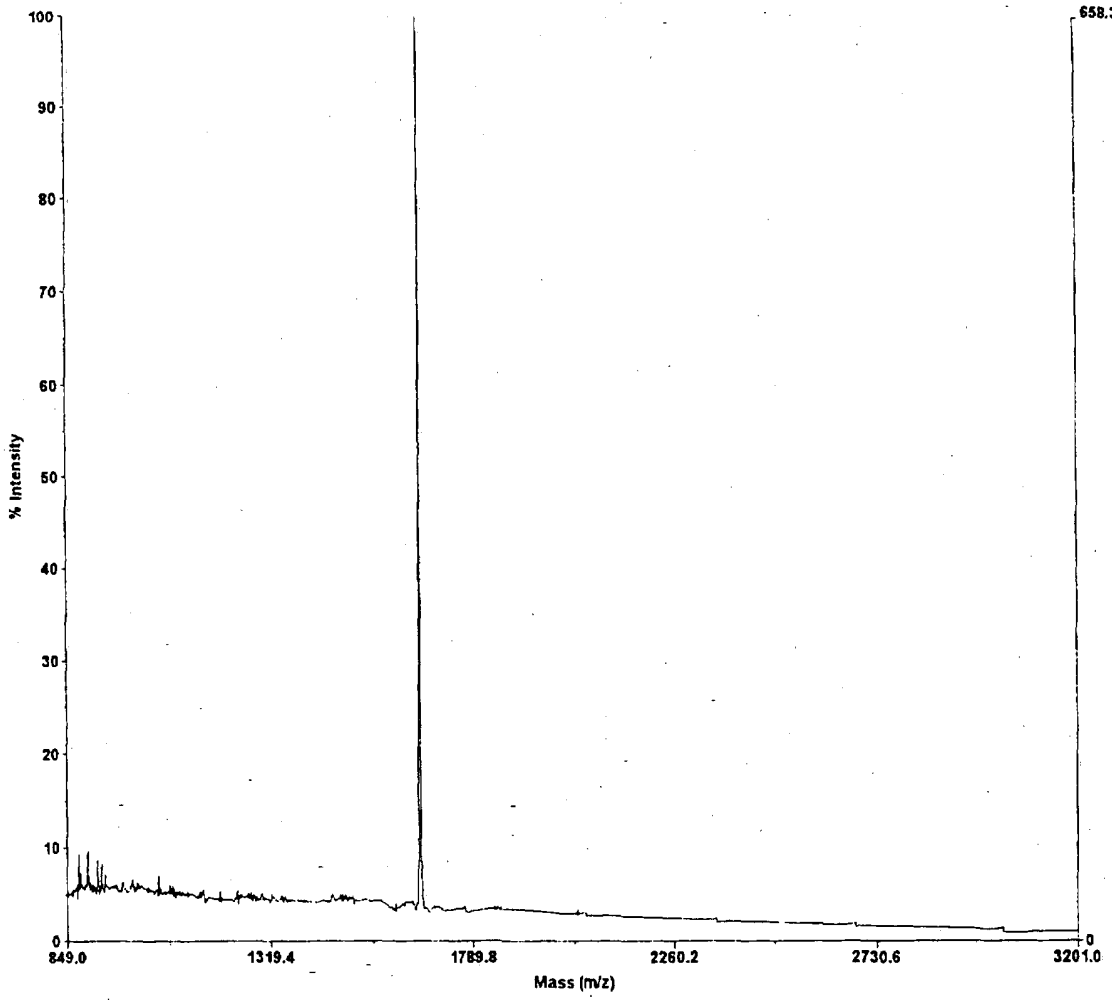
FIG. 16

FIG. 17

GFI-107
Applicant: Stephen Hamilton Filed: Herewith
Application No.: To Be Assigned
For : EXPRESSION OF CLASS 2 MANNOSIDASE AND CLASS III MANNOSIDASE IN LOWER EUKARYOTIC CELLS
24/47

Applied Biosystems Voyager System 1246

Voyager Spec #1=>BC=>NR(2.00)[BP = 1664.6, 658]



658.3

Mode of operation:	Linear
Extraction mode:	Delayed
Polarity:	Positive
Acquisition control:	Manual
Accelerating voltage:	20000 V
Grid voltage:	94%
Guide wire 0:	0.05%
Extraction delay time:	100 nsec
Acquisition mass range:	850 – 3200 Da
Number of laser shots:	100/spectrum
Laser intensity:	2713
Laser Rep Rate:	20.0 Hz
Calibration type:	Default
Calibration matrix:	2,5-Dihydroxybenzoic acid
Low mass gate:	800 Da
Digitizer start time:	18.582
Bin size:	2 nsec
Number of data points:	8676
Vertical scale:	500 mV
Vertical offset:	0%
Input bandwidth:	150 MHz
Sample well:	47
Plate ID:	100 WELL PLATE
Serial number:	1246
Instrument name:	Voyager-DE
Plate type filename:	C:\VOYAGER\100 well plate.p
Lab name:	PE Biosystems
Absolute x-position:	31305.6
Absolute y-position:	28069.3
Relative x-position:	-761.913
Relative y-posititon:	1081.83
Shots in spectrum:	100
Source pressure:	4.393e-007
Mirror pressure:	0
TC2 pressure:	0.004253
TIS gate width:	30
TIS flight length:	940

Acquired: 10:12:00, June 13, 2003

Printed: 08:41, June 16, 2003

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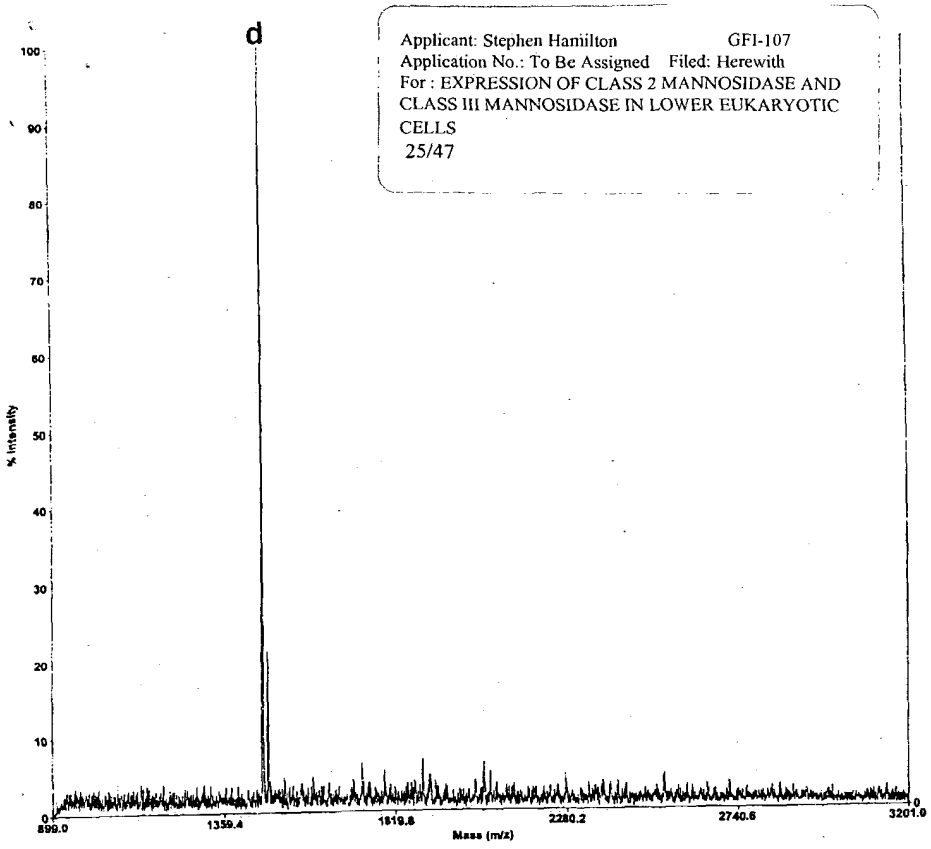
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90
80
70
60
50
40
30
20
10
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1359.4
1819.8
2280.2
2740.6
3201.0
Mass (m/z)

FIG. 18

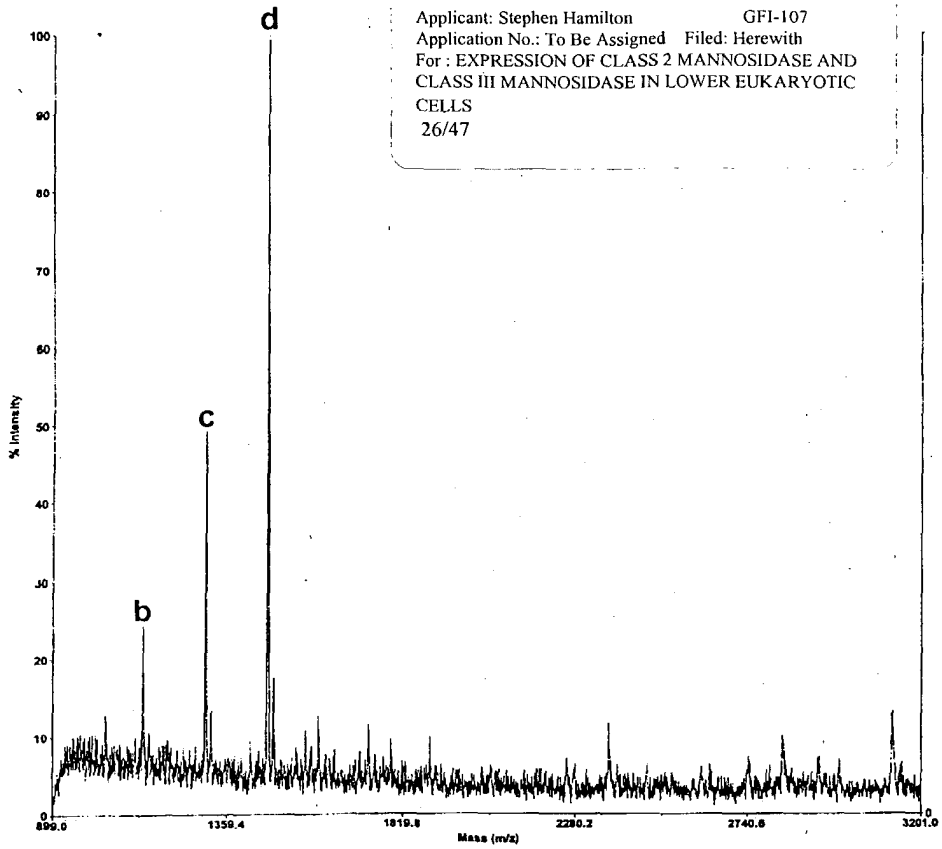

d
c
b
% Intensity
100
90
80
70
60
50
40
30
20
10
0
899.0
1359.4
1819.8
2280.2
2740.6
3201.0
Mass (m/z)

FIG. 19

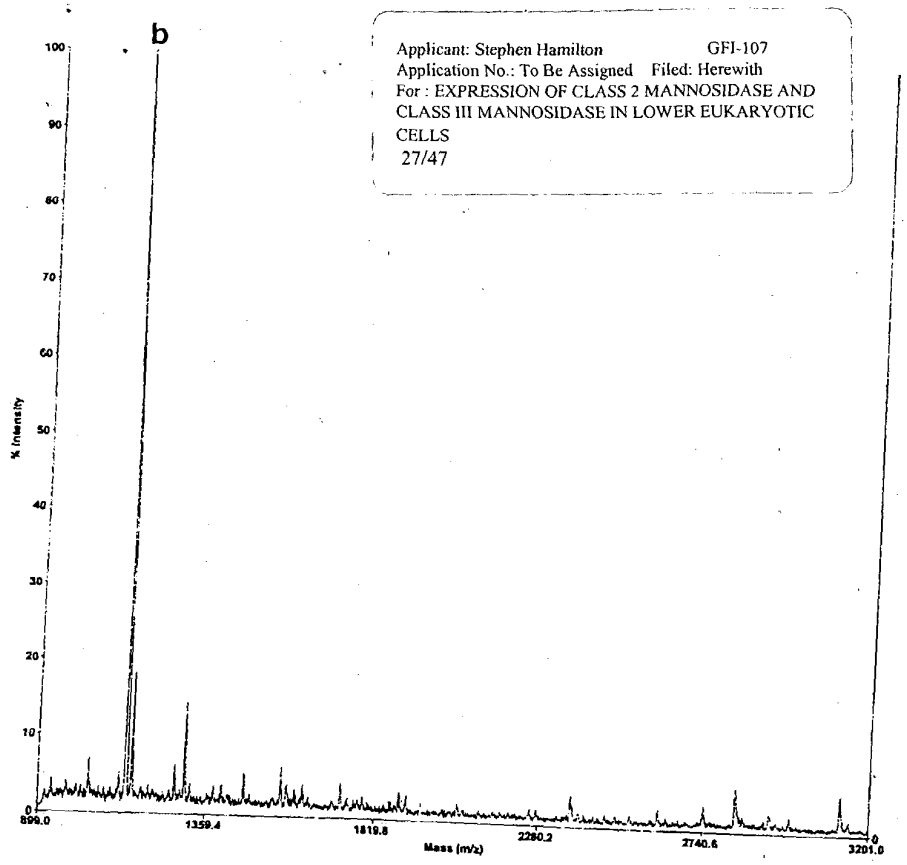

b
100
90
80
70
60
50
40
30
20
10
0
% Intensity
899.0
1359.4
1819.8
2280.2
2740.6
3201.0
Mass (m/z)

FIG. 20

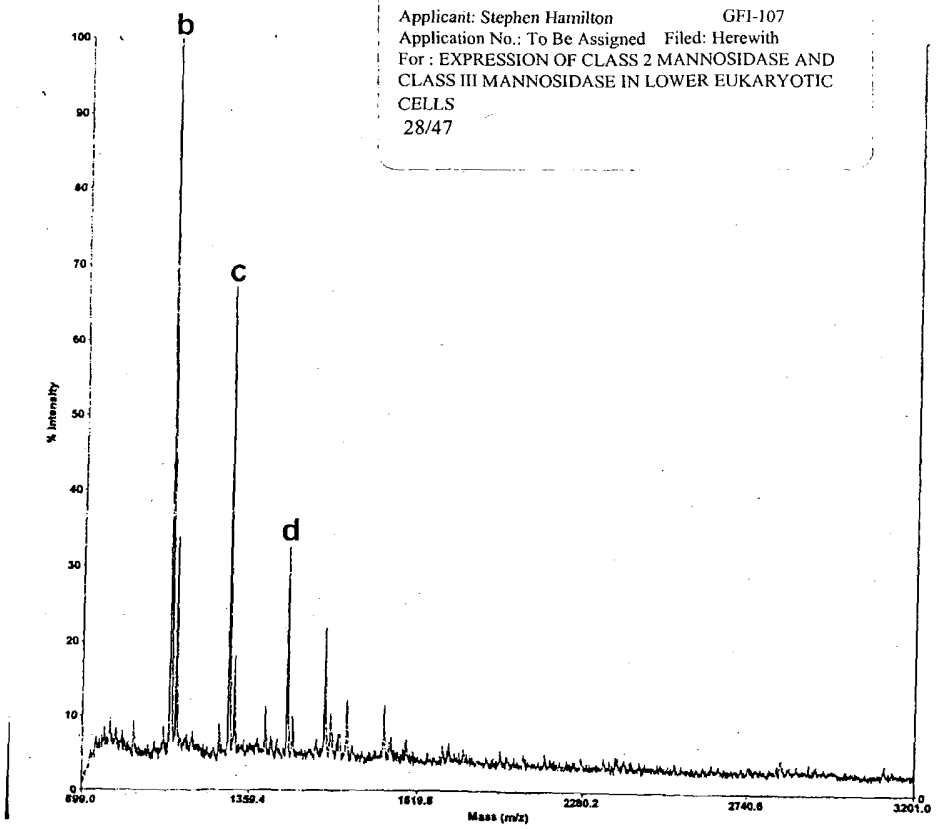
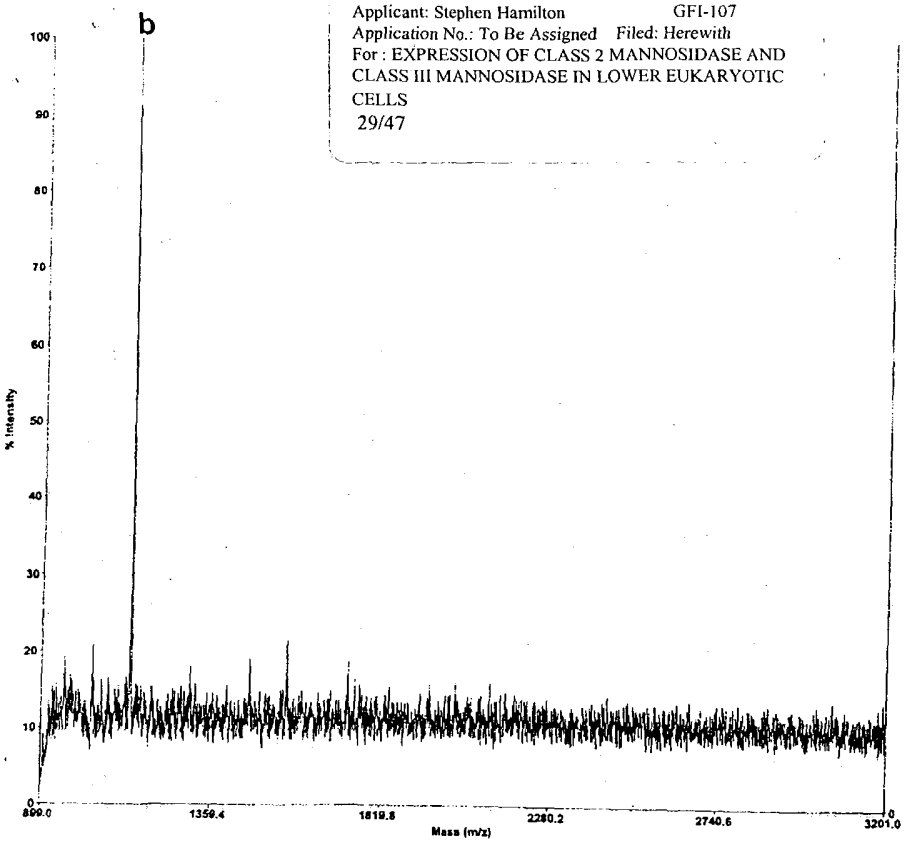

b
c
d
% Intensity
Mass (m/z)
100
90
80
70
60
50
40
30
20
10
0
899.0
1359.4
1819.8
2280.2
2740.6
3201.0

FIG. 21


b
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90
80
70
60
50
40
30
20
10
0
% Intensity
899.0
1359.4
1819.8
2280.2
2740.6
3201.0
Mass (m/z)

FIG. 22

FIG. 23

Biology WorkBench

click here to toggle between menus and buttons

WE Moved! http://workbench.sdsc.edu/

Version 3.2

BOXSHADE

Color-Coded Plots of Pre-Aligned Sequences

Selected Sequence(s)

- Droso MannII (X77652),

C.elegans MannII,
rMannII (XM_218816.1),
hMannIIx D55649,
Mouse MannII (X61172),
human MannII (U31520),
CionaMannII (AK116684),
ArabMannII,
Insect ManIII,
hLyso MannII,
hCyto MannII (NM_006715)

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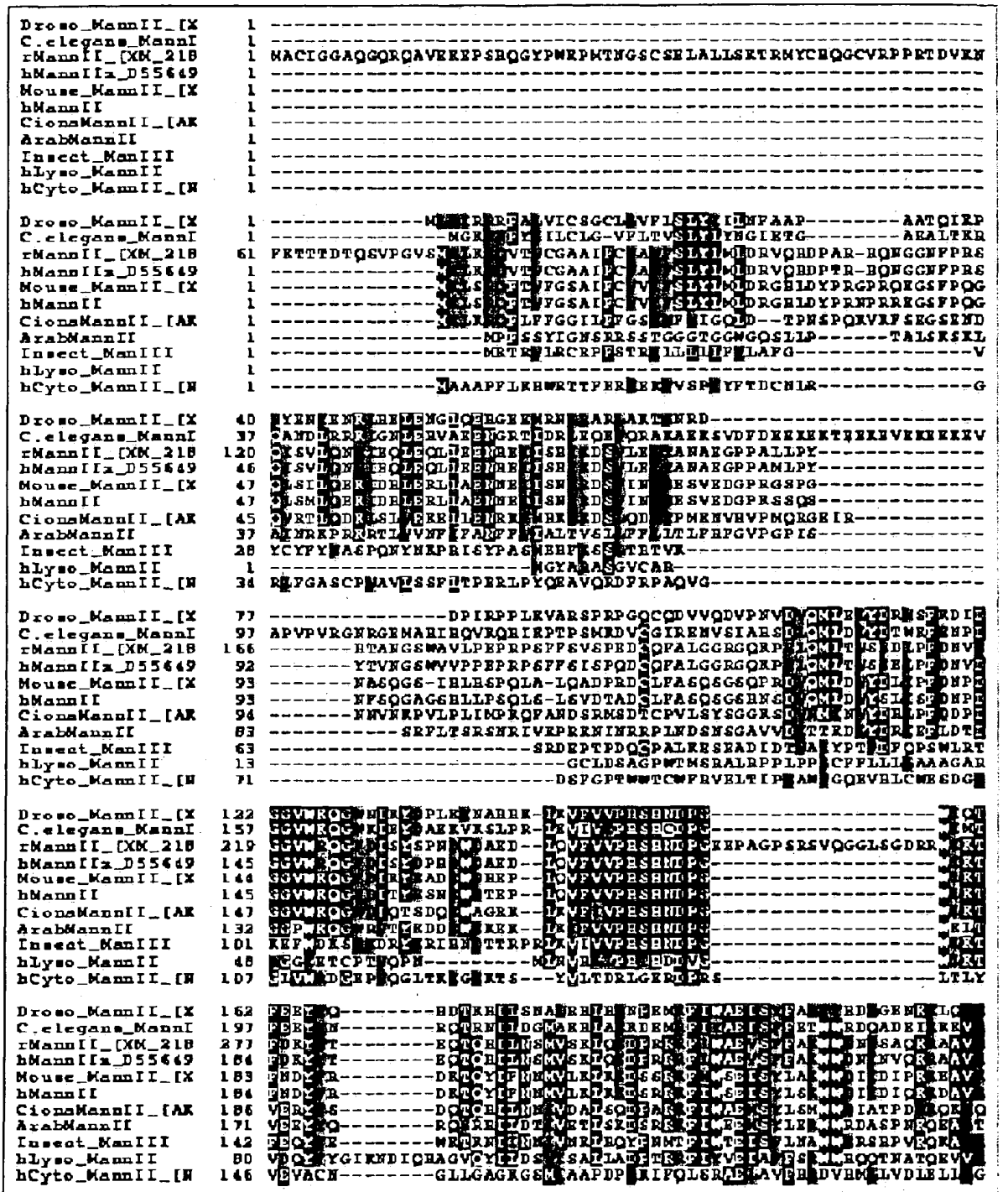
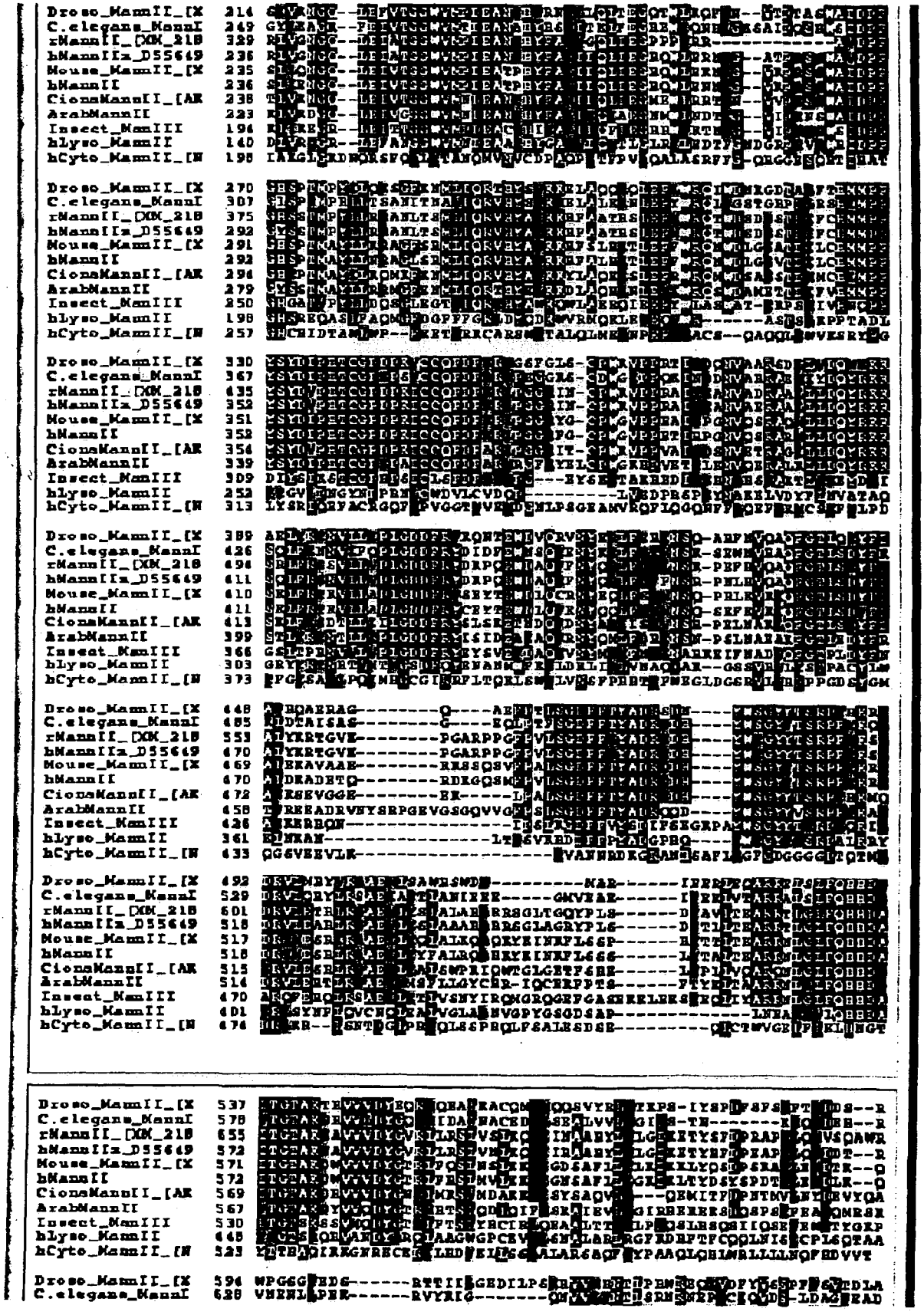
Download a PostScript version of the output

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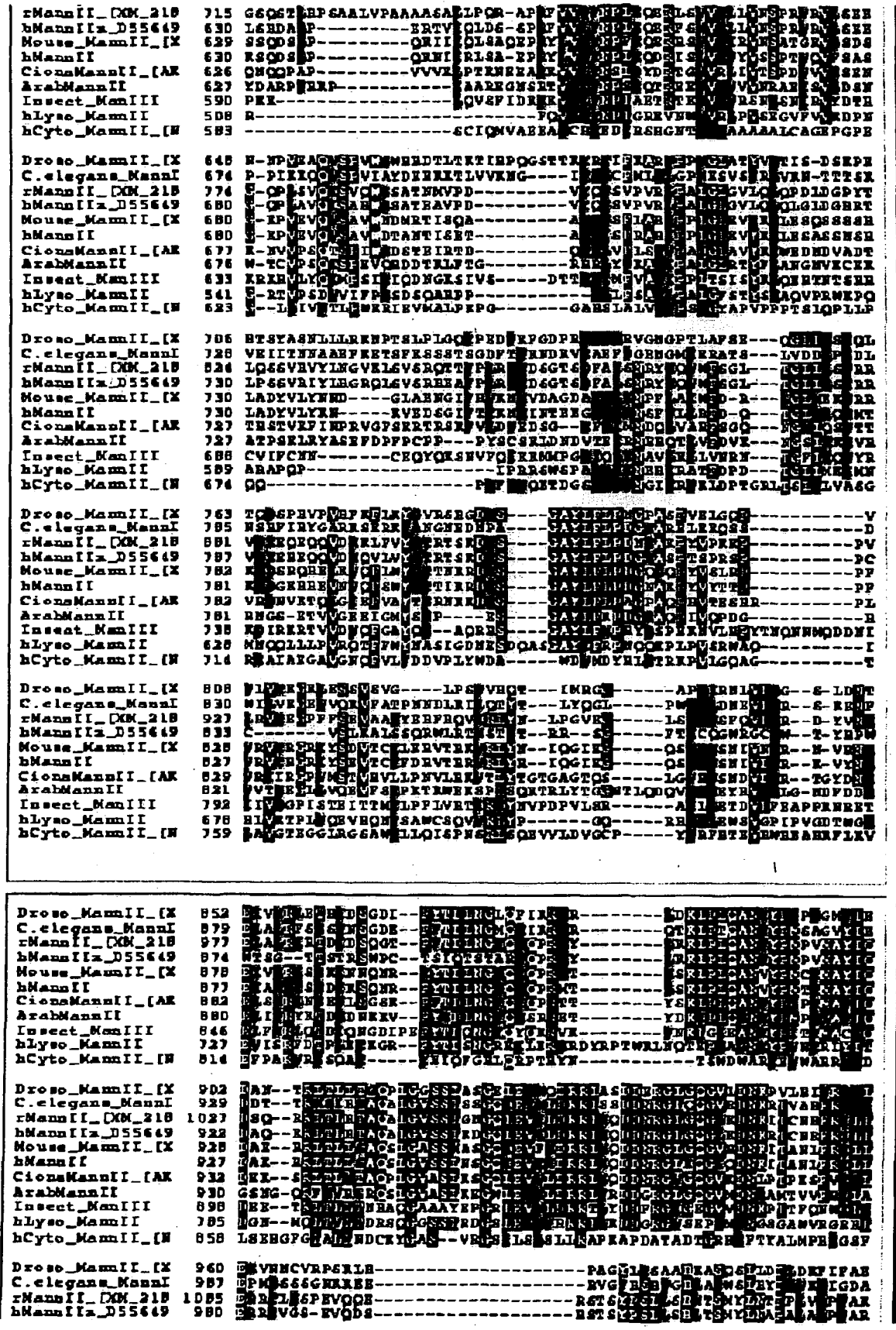
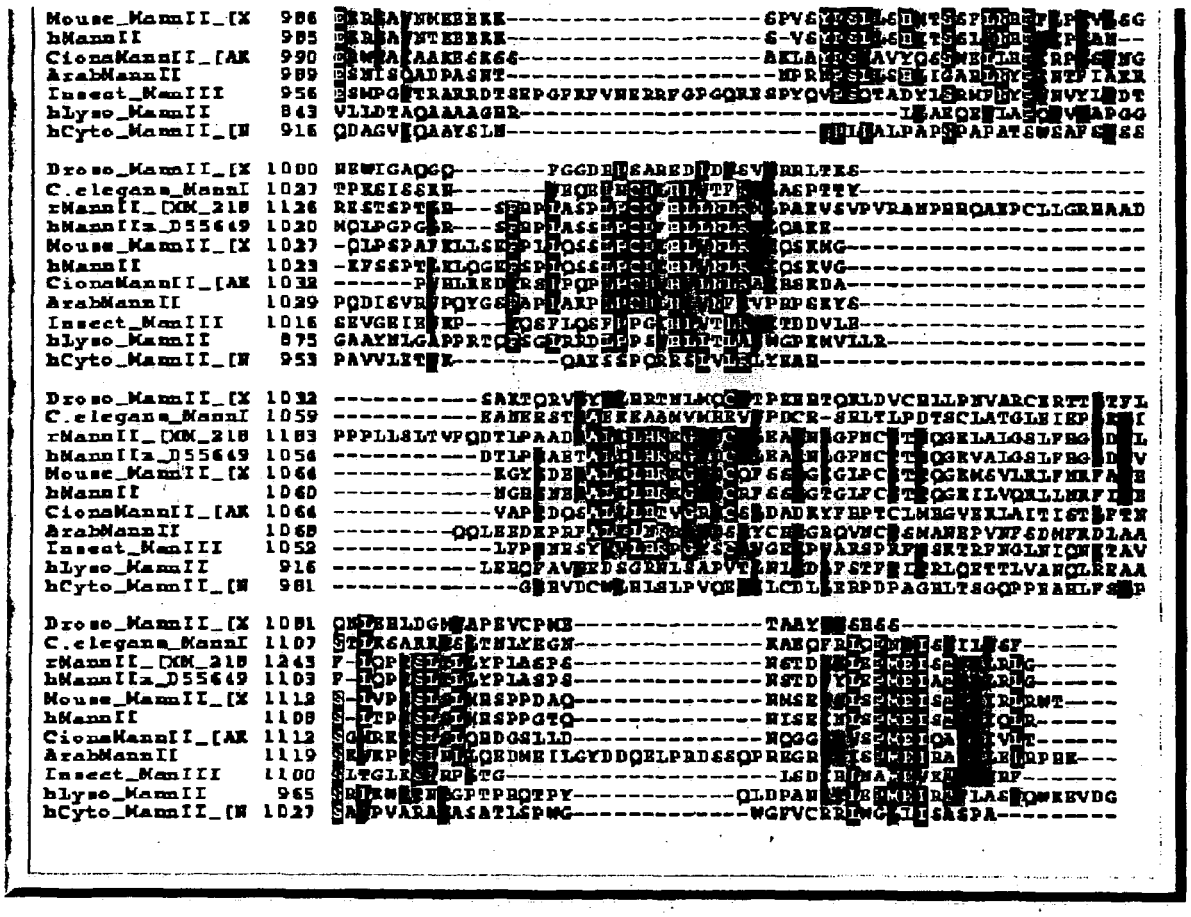
C.elegans_MannI
rMannII_[XM_218
hMannIIx_D55649
Mouse_MannII_[X
hMannII
CionaMannII_[AR
ArabMannII
Insect_MannIII
hLyso_MannII
hCyto_MannII_[N





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Citation

Algorithm Citation:

Not given, but presumably Kay Hofmann and Michael D. Baron.

Program Citation:

Boxshade version 3.3.1, by Kay Hofmann and Michael D. Baron.

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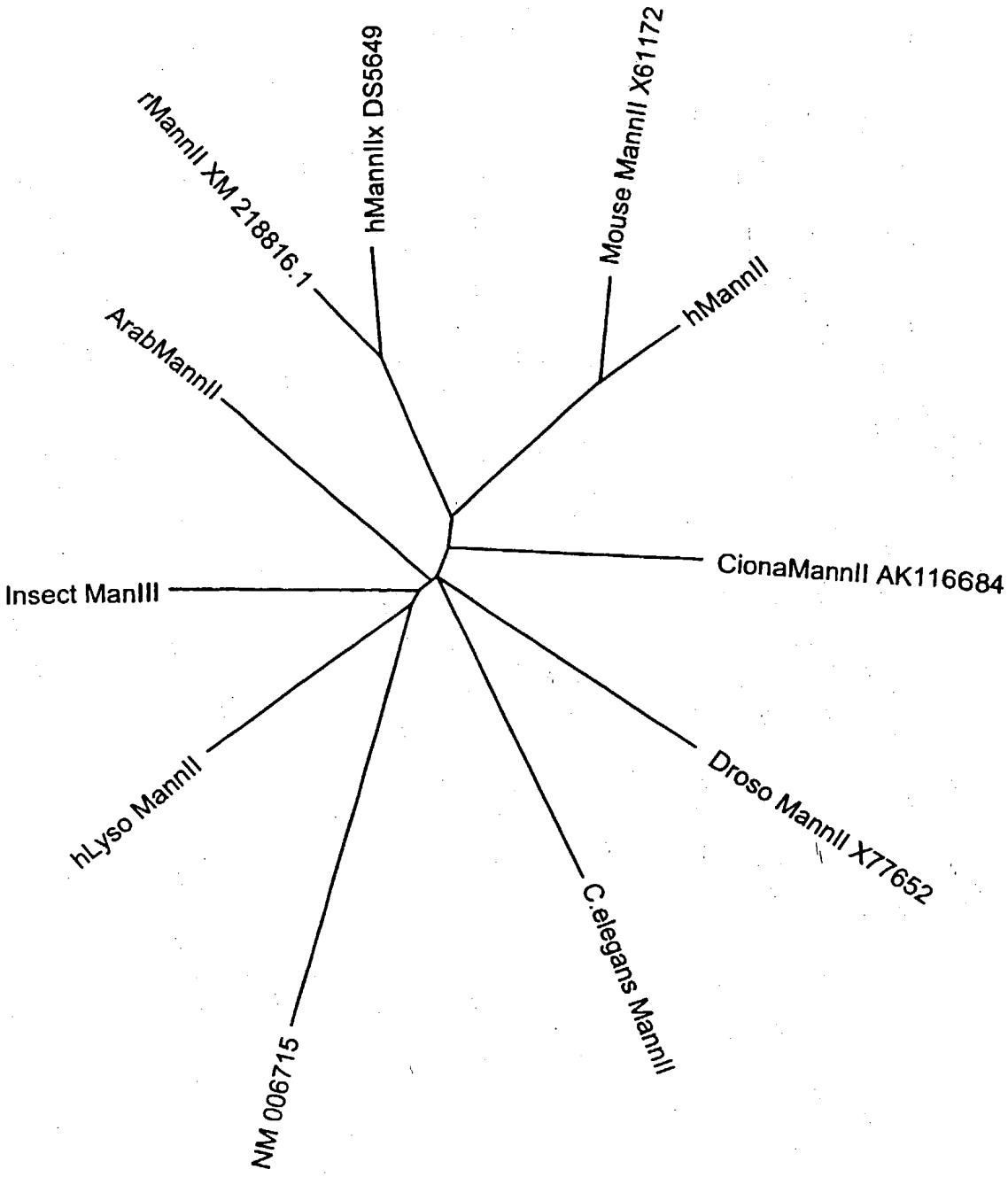
FIG. 24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hMannIIx DS5649
Mouse MannII X61172
hMannII
ArabMannII
CionaMannII AK116684
Insect ManIII
hLyso MannII
Droso MannII X77652
C.elegans MannII
NM 006715

FIG. 25

Arabidopsis thaliana Mannosidase II (NM_121499)

```
   1 ATGCCGTTCTCCTCGTATATCGGCAACAGCCGCCGTAGCTCCACCGGCGGAGGAACCGGCGGTTGGGGCCAATCTCTTCTTCCAACAGCGTTATCAAAGTCAAAACTAG
   1 M  P  F  S  S  Y  I  G  N  S  R  R  S  S  T  G  G  G  T  G  G  W  G  Q  S  L  L  P  T  A  L  S  K  S  K  L
 110 CGATCAATCGAAAACCACGAAAACGAACTCTCGTAGTCAATTTCATCTTCGCCAACTTCTTCGTCATCGCACTCACCGTCTCACTCCTCTTCTTCCTCCTCACTCTCTT
  37 A  I  N  R  K  P  R  K  R  T  L  V  V  N  F  I  F  A  N  F  F  V  I  A  L  T  V  S  L  L  F  F  L  L  T  L  F
 219 CCACTTCGGCGTACCAGGACCGATCTCCTCACGATTCCTTACCTCCAGATCCAATCGGATCGTCAAGCCACGGAAGAATATTAATCGCCGACCCTTAAACGATTCCAAT
  73 H  F  G  V  P  G  P  I  S  S  R  F  L  T  S  R  S  N  R  I  V  K  P  R  K  N  I  N  R  R  P  L  N  D  S  N
 328 TCAGGCGCCGTCGTTGATATCACAACTAAAGATCTATACGATAGGATTGAGTTTCTTGATACAGATGGTGGTCCATGGAAACAAGGTTGGAGAGTTACGTATAAAGACG
 110 S  G  A  V  V  D  I  T  T  K  D  L  Y  D  R  I  E  F  L  D  T  D  G  G  P  W  K  Q  G  W  R  V  T  Y  K  D
 437 ATGAGTGGGAGAAAGAGAAGCTCAAAATCTTCGTTGTTCCTCATTCTCATAACGATCCTGGTTGGAAATTGACTGTAGAGGAGTATTATCAGAGACAATCCAGACATAT
 146 D  E  W  E  K  E  K  L  K  I  F  V  V  P  H  S  H  N  D  P  G  W  K  L  T  V  E  E  Y  Y  Q  R  Q  S  R  H  I
 546 TCTTGACACCATTGTTGAGACTTTATCTAAGGATTCAAGAAGAAAGTTTATATGGGAGGAGATGTCATATCTGGAGAGATGGTGGAGAGACGCTTCACCTAATAAACAA
 182 L  D  T  I  V  E  T  L  S  K  D  S  R  R  K  F  I  W  E  E  M  S  Y  L  E  R  W  W  R  D  A  S  P  N  K  Q
 655 GAAGCTTTGACTAAATTGGTTAAGGATGGGCAGCTAGAGATTGTTGGAGGTGGCTGGGTTATGAATGATGAGGCTAATTCACATTATTTTGCCATAATTGAACAGATAG
 219 E  A  L  T  K  L  V  K  D  G  Q  L  E  I  V  G  G  G  W  V  M  N  D  E  A  N  S  H  Y  F  A  I  I  E  Q  I
 764 CAGAGGGTAATATGTGGCTGAATGACACAATTGGGGTTATTCCTAAGAATTCTTGGGCTATAGATCCCTTTGGCTATTCATCAACCATGGCTTATCTTCTCCGGCGTAT
 255 A  E  G  N  M  W  L  N  D  T  I  G  V  I  P  K  N  S  W  A  I  D  P  F  G  Y  S  S  T  M  A  Y  L  L  R  R  M
 873 GGGTTTTGAAAACATGCTTATTCAAAGGACTCATTACGAGCTCAAGAAAGACCTTGCCCAGCATAAGAATCTTGAATATATTTGGCGTCAGAGCTGGGATGCTATGGAA
 291 G  F  E  N  M  L  I  Q  R  T  H  Y  E  L  K  K  D  L  A  Q  H  K  N  L  E  Y  I  W  R  Q  S  W  D  A  M  E
 982 ACCACAGATATCTTTGTTCATATGATGCCGTTTTATTCATACGATATCCCACACACTTGTGGACCAGAGCCTGCAATTTGCTGTCAGTTTGATTTCGCTCGGATGCGGG
 328 T  T  D  I  F  V  H  M  M  P  F  Y  S  Y  D  I  P  H  T  C  G  P  E  P  A  I  C  C  Q  F  D  F  A  R  M  R
1091 GATTTAAGTATGAACTTTGTCCATGGGGAAAGCACCCAGTGGAGACCACACTAGAAAATGTGCAGGAGAGGGCATTAAAGCTTCTGGATCAATACAGGAAAAAATCCAC
 364 G  F  K  Y  E  L  C  P  W  G  K  H  P  V  E  T  T  L  E  N  V  Q  E  R  A  L  K  L  L  D  Q  Y  R  K  K  S  T
1200 TCTATATCGAACTAATACACTTCTTATACCTCTTGGAGATGATTTTAGGTACATTAGTATCGATGAAGCCGAGGCTCAGTTCCGTAACTACCAGATGTTGTTTGATCAC
 400 L  Y  R  T  N  T  L  L  I  P  L  G  D  D  F  R  Y  I  S  I  D  E  A  E  A  Q  F  R  N  Y  Q  M  L  F  D  H
1309 ATCAACTCTAATCCTAGTCTAAACGCAGAAGCAAAGTTTGGTACTTTGGAGGATTATTTCAGAACAGTCCGAGAAGAAGCAGACACAGAGTGAATTATTCTCGTCCTGGTG
 437 I  N  S  N  P  S  L  N  A  E  A  K  F  G  T  L  E  D  Y  F  R  T  V  R  E  E  A  D  R  V  N  Y  S  R  P  G
1418 AGGTTGGCTCTGGTCAGGTTGTTGGTTTCCCTTCTCTGTCAGGTGACTTCTTTACATATGCAGATAGGCAACAAGACTATTGGAGTGGTTATTATGTTTCAAGACCTTT
 473 E  V  G  S  G  Q  V  V  G  F  P  S  L  S  G  D  F  F  T  Y  A  D  R  Q  Q  D  Y  W  S  G  Y  Y  V  S  R  P  F
1527 CTTCAAAGCTGTTGATCGTGTGCTCGAGCATACCCTTCGTGGAGCTGAGATCATGATGTCATTTCTGCTAGGTTATTGCCATCGAATTCAATGTGAGAAATTTCCAACA
 509 F  K  A  V  D  R  V  L  E  H  T  L  R  G  A  E  I  M  M  S  F  L  L  G  Y  C  H  R  I  Q  C  E  K  F  P  T
1636 AGTTTTACGTATAAGTTGACTGCTGCAAGAAGAAATCTGGCTCTTTTCCAGCACCATGATGGGGTAACTGGAACTGCTAAGGATTATGTGGTACAAGATTACGGCACCC
 546 S  F  T  Y  K  L  T  A  A  R  R  N  L  A  L  F  Q  H  H  D  G  V  T  G  T  A  K  D  Y  V  V  Q  D  Y  G  T
1745 GGATGCATACTTCATTGCAAGACCTTCAGATCTTTATGTCTAAAGCAATCGAAGTTCTTCTTGGGATCCGCCACGAGAAAGAAAAATCTGATCAATCCCCATCATTTTT
 582 R  M  H  T  S  L  Q  D  L  Q  I  F  M  S  K  A  I  E  V  L  L  G  I  R  H  E  K  E  K  S  D  Q  S  P  S  F  F
1854 CGAGGCAGAGCAAATGAGATCAAAGTATGATGCTCGGCCAGTTCACAAGCCAATTGCTGCCCGGGAAGGAAATTCGCACACAGTTATACTCTTCAATCCATCAGAACAG
 618 E  A  E  Q  M  R  S  K  Y  D  A  R  P  V  H  K  P  I  A  A  R  E  G  N  S  H  T  V  I  L  F  N  P  S  E  Q
1963 ACGAGAGAGGAGGTGGTGACGGTTGTTGTTAACCGCGCTGAAATCTCGGTTTTGGACTCAAACTGGACTTGTGTCCCTAGCCAAATTTCTCCTGAAGTGCAGCATGACG
 655 T  R  E  E  V  V  T  V  V  V  N  R  A  E  I  S  V  L  D  S  N  W  T  C  V  P  S  Q  I  S  P  E  V  Q  H  D
2072 ATACCAAACTATTCACCGGCAGACATCGCCTTTACTGGAAAGCTTCCATCCCAGCTCTTGGTCTGAGAACATATTTCATTGCTAATGGGAATGTCGAGTGTGAGAAAGC
 691 D  T  K  L  F  T  G  R  H  R  L  Y  W  K  A  S  I  P  A  L  G  L  R  T  Y  F  I  A  N  G  N  V  E  C  E  K  A
2181 TACTCCGTCTAAACTCAAATACGCTTCTGAGTTTGACCCATTTCCTTGTCCTCCTCCATATTCCTGCTCCAAACTGGACAACGACGTTACTGAGATCCGAAATGAACAT
 727 T  P  S  K  L  K  Y  A  S  E  F  D  P  F  P  C  P  P  P  Y  S  C  S  K  L  D  N  D  V  T  E  I  R  N  E  H
2290 CAGACTCTTGTGTTTGATGTGAAGAACGGATCACTGCGGAAGATAGTCCATAGAAACGGATCAGAGACTGTTGTGGGAGAAGAGATAGGTATGTACTCTAGTCCAGAGA
 764 Q  T  L  V  F  D  V  K  N  G  S  L  R  K  I  V  H  R  N  G  S  E  T  V  V  G  E  E  I  G  M  Y  S  S  P  E
2399 GTGGAGCTTACCTGTTCAAACCAGATGGTGAAGCTCAGCCAATTGTTCAACCTGATGGACATGTAGTCACCTCTGAGGGTCTGCTGGTTCAAGAAGTCTTCTCTTACCC
 800 S  G  A  Y  L  F  K  P  D  G  E  A  Q  P  I  V  Q  P  D  G  H  V  V  T  S  E  G  L  L  V  Q  E  V  F  S  Y  P
2508 TAAAACCAAATGGGAGAAATCACCCCTCTCTCAGAAAACTCGTCTTTACACTGGAGGTAATACGCTTCAGGATCAAGTGGTCGAGATAGAAATATCATGTTGAGCTTCTT
 836 K  T  K  W  E  K  S  P  L  S  Q  K  T  R  L  Y  T  G  G  N  T  L  Q  D  Q  V  V  E  I  E  Y  H  V  E  L  L
2617 GGTAATGATTTTGATGACCGGGAATTGATTGTCCGGTACAAGACTGATGTTGACAACAAGAAGGTCTTCTATTCAGATCTCAATGGTTTCCAAATGAGCAGGAGAGAAA
 873 G  N  D  F  D  D  R  E  L  I  V  R  Y  K  T  D  V  D  N  K  K  V  F  Y  S  D  L  N  G  F  Q  M  $  R  R  E
2726 CTTATGATAAGATCCCTCTTCAAGGAAACTACTACCCAATGCCATCTCTCGCATTTATCCAAGGATCCAATGGTCAGAGATTCTCCGTGCACTCTCGTCAATCTCTCGG
 909 T  Y  D  K  I  P  L  Q  G  N  Y  Y  P  M  P  S  L  A  F  I  Q  G  S  N  G  Q  R  F  S  V  H  S  R  Q  S  L  G
2835 TGTTGCAAGCCTCAAAGAGGGTTGGTTGGAGATTATGCTGGACAGACGGTTGGTTCGTGATGACGGACGGGGTCTAGGGCAAGGTGTGATGGATAACCGCGCAATGACC
 945 V  A  S  L  K  E  G  W  L  E  I  M  L  D  R  R  L  V  R  D  D  G  R  G  L  G  Q  G  V  M  D  N  R  A  M  T
2944 GTGGTATTTCACCTTCTTGCGGAATCTAACATTTCTCAAGCAGACCCTGCTTCCAACACTAACCCGAGGAACCCTTCGCTTCTCTCTCACCTCATAGGTGCTCACTTAA
 982 V  V  F  H  L  L  A  E  S  N  I  S  Q  A  D  P  A  S  N  T  N  P  R  N  P  S  L  L  S  H  L  I  G  A  H  L
3053 ACTACCCCATAAACACATTCATTGCCAAGAAACCGCAAGACATATCTGTGCGTGTTCCACAATACGGTTCCTTTGCTCCTTTAGCCAAACCGTTACCATGTGACCTCCA
1018 N  Y  P  I  N  T  F  I  A  K  K  P  Q  D  I  S  V  R  V  P  Q  Y  G  S  F  A  P  L  A  K  P  L  P  C  D  L  H
3162 CATTGTAAATTTCAAGGTTCCTCGTCCATCCAAATACTCTCAGCAATTGGAAGAAGACAAGCCAAGGTTCGCTCTTATCCTCAATAGACGAGCTTGGGATTCAGCTTAT
1054 I  V  N  F  K  V  P  R  P  S  K  Y  S  Q  Q  L  E  E  D  K  P  R  F  A  L  I  L  N  R  R  A  W  D  S  A  Y
3271 TGCCATAAAGGAAGACAAGTAAACTGCACAAGCATGGCTAATGAACCAGTAAACTTTTCCGACATGTTCAAAGATCTTGCAGCTTCAAAGGTAAAACCAACTTCACTGA
1091 C  H  K  G  R  Q  V  N  C  T  S  M  A  N  E  P  V  N  F  S  D  M  F  K  D  L  A  A  S  K  V  K  P  T  S  L
3380 ATCTCTTGCAAGAAGATATGGAGATTCTTGGGTACGATGACCAAGAGCTACCTCGAGATAGTTCACAGCCACGGGAAGGACGTGTCTCGATCTCTCCCATGGAAATACG
1127 N  L  L  Q  E  D  M  E  I  L  G  Y  D  D  Q  E  L  P  R  D  S  S  Q  P  R  E  G  R  V  S  I  S  P  M  E  I  R
3489 AGCTTATAAGCTTGAACTGCGACCTCACAAGTGA
1163 A  Y  K  L  E  L  R  P  H  K
```

FIG. 26

C. elegans Mannosidase II (NM_073594)

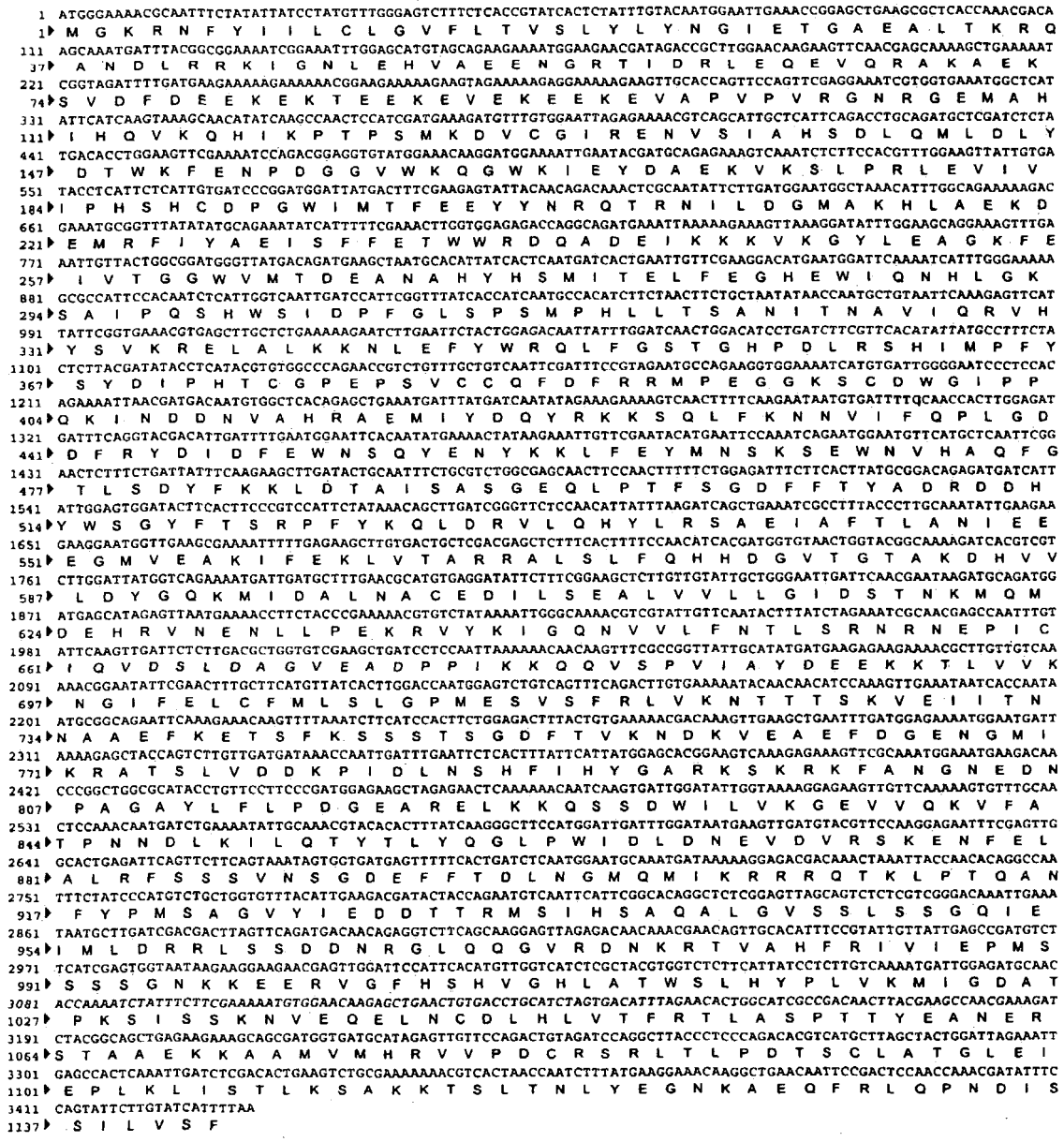

FIG. 27

Ciona intestinalis mannosidase II (AK116684)

```
   1 ATGAAGCTCAAACGCCAGTTCTTATTCTTTGGTGGAATTCTGTTCTTCGGGAGTATCTGGTTTATGATAGGTCAACTTGACACTCCTAATTCGCCACAGAAAGTCAAAT
   1 M  K  L  K  R  Q  F  L  F  F  G  G  I  L  F  F  G  S  I  W  F  M  I  G  Q  L  D  T  P  N  S  P  Q  K  V  K
 110 TCTCGGAAGGCAGTGAAAATGACCAAGTTCGAACCCTTCAAGACAAACTTAGTCTGGTGGAAAAAGAATTGTTAGAAAATCGTAAAATAATGCACAAGGTGAAAGATAG
  37 F  S  E  G  S  E  N  D  Q  V  R  T  L  Q  D  K  L  S  L  V  E  K  E  L  L  E  N  R  K  I  M  H  K  V  K  D  S
 219 TCTACAGGATATGACACCCATGAAAAATGTTCATGTGCCTATGCAGCGCGGAGAAATAAGAAACAACGTCAATAAACCTGTGCTACCACTTATAATGCCCAAGCAATTT
  73 L  Q  D  M  T  P  M  K  N  V  H  V  P  M  Q  R  G  E  I  R  N  N  V  N  K  P  V  L  P  L  I  M  P  K  Q  F
 328 GCGAATGACTCCCGAATGAGTGACACGTGTCCTGTGCTCTCGTACTCCGGTGGCAAGTCCGATGTTAACATGATTAACGTGTATGATCATCTTCCATTTGATGATCCAG
 110 A  N  D  S  R  M  S  D  T  C  P  V  L  S  Y  S  G  G  K  S  D  V  N  M  I  N  V  Y  D  H  L  P  F  D  D  P
 437 ATGGTGGAGTTTGGAAACAAGGTTGGGACATCCAGACATCGGATCAGGAATGGGCTGGGAGAAAATTGAAAGTGTTCATTGTCCCTCACTCACATAATGATCCTGGTTG
 146 D  G  G  V  W  K  Q  G  W  D  I  Q  T  S  D  Q  E  W  A  G  R  K  L  K  V  F  I  V  P  H  S  H  N  D  P  G  W
 546 GTTAAAGACGGTGGAAAGATACTTCAGCGATCAAACACAACATATTCTCAATAATATTGTGGATGCTTTGAGTCAAGACCCTGCAAGGAAGTTTATCTGGGCAGAGATG
 182 L  K  T  V  E  R  Y  F  S  D  Q  T  Q  H  I  L  N  N  I  V  D  A  L  S  Q  D  P  A  R  K  F  I  W  A  E  M
 655 TCGTATCTCTCAATGTGGTGGGACATTGCCACACCTGATCGTAAGCAGAAAATGCAGACACTCGTGAAGAATGGACAGCTTGAGATAGTTACGGGTGGTTGGGTCATGA
 219 S  Y  L  S  M  W  W  D  I  A  T  P  D  R  K  Q  K  M  Q  T  L  V  K  N  G  Q  L  E  I  V  T  G  G  W  V  M
 764 ATGATGAAGCAAACACTCATTACTTTGCTATGATTGATCAACTCATTGAAGGTATGGAATGGTTGAGGCGAACATTGAATGTTGTTCCAAAAAGTGGGTGGGCGATTGA
 255 N  D  E  A  N  T  H  Y  F  A  M  I  D  Q  L  I  E  G  M  E  W  L  R  R  T  L  N  V  V  P  K  S  G  W  A  I  D
 873 TCCCTTTGGTCACACCCCCACCATGGCTTATATACTGAAACAGATGAAGTTCAAAAACATGCTGATACAAAGAGTCCATTATGCAGTGAAGAAGTATCTTGCTCAGGAA
 291 P  F  G  H  T  P  T  M  A  Y  I  L  K  Q  M  K  F  K  N  M  L  I  Q  R  V  H  Y  A  V  K  K  Y  L  A  Q  E
 982 AAGTCTCTGGAATTCAGATGGAGACAAATGTGGGATTCAGCTTCAAGTACAGACATGATGTGTCATCTCATGCCTTTCTATTCATATGATGTTCCTCATACTTGTGGCC
 328 K  S  L  E  F  R  W  R  Q  M  W  D  S  A  S  S  T  D  M  M  C  H  L  M  P  F  Y  S  Y  D  V  P  H  T  C  G
1091 CAGACCCCAAGATTTGCTGCCAGTTTGATTTGCTCGCTTACCCGGCGGCAAGATAACCTGCCCATGGAAAGTTCCTCCTGTTGCCATCACTGACTCCAATGTAGAAAC
 364 P  D  P  K  I  C  C  Q  F  D  F  A  R  L  P  G  G  K  I  T  C  P  W  K  V  P  P  V  A  I  T  D  S  N  V  E  T
1200 ACGAGCCGGAATACTACTTGACCAATATAGAAAAAAGTCAAAACTCTTCAAAAGTGACACCCTGCTTATTATATTAGGAGATGATTTTCGTTATTCGCTGAGCAAGGAA
 400 R  A  G  I  L  L  D  Q  Y  R  K  K  S  K  L  F  K  S  D  T  L  L  I  I  L  G  D  D  F  R  Y  S  L  S  K  E
1309 ACCAACGATCAGTTTGACAACTACGCTCGAATTATCTCGTATGTGAATTCGCACCCAGAGTTAAACGCAAAACTTCAGTTTGGAACATTATCCGAATATTTTGATGCCA
 437 T  N  D  Q  F  D  N  Y  A  R  I  I  S  Y  V  N  S  H  P  E  L  N  A  K  L  Q  F  G  T  L  S  E  Y  F  D  A
1418 TGAAATCTGAAGTGGGGGGAGAGGAAAAACTCCCAGCTTTAAGTGGTGATTTCTTCACTTATGCTGATAGAGAAGATCACTATTGGAGTGGTTACTACACTTCACGGCC
 473 M  K  S  E  V  G  G  E  E  K  L  P  A  L  S  G  D  F  F  T  Y  A  D  R  E  D  H  Y  W  S  G  Y  Y  T  S  R  P
1527 TTACCACAAAATGCAGGAGAGAGTCCTGGAAAGCCACCTTCGAGGAGCAGAAATGTTGTTTGCGCTCTCATGGCCCAAAATCCAGTGGACAGGACTTGGTGAAACATTT
 509 Y  H  K  M  Q  E  R  V  L  E  S  H  L  R  G  A  E  M  L  F  A  L  S  W  P  K  I  Q  W  T  G  L  G  E  T  F
1636 TCACATGAACTTTACCCACTGCTGGTCCAAGCACGTCAAAATCTTGGTTTGTTTCAACACCACGATGGTATAACAGGCACAGCAAAGGATCATGTTGTTGTTGATTACG
 546 S  H  E  L  Y  P  L  L  V  Q  A  R  Q  N  L  G  L  F  Q  H  H  D  G  I  T  G  T  A  K  D  H  V  V  V  D  Y
1745 GGAATAAACTCATGAAGAGTGTTATGGATGCAAAGAAGGTAATTTCATACAGTGCCCAAGTTCTGTTGCAAGAAATGATCACGTTTGATCCAAATACCATGGTACTTAA
 582 G  N  K  L  M  K  S  V  M  D  A  K  K  V  I  S  Y  S  A  Q  V  L  L  Q  E  M  I  T  F  D  P  N  T  M  V  L  N
1854 CTATGATGAGGTGTATCAAGCTCAGAACCAACAACCTGCGCCTGTGGTTGTTAAGCTACCAACGAAGAATGAAGAAGCGCGGAAAGTCGTTCTCTACAACTCTCTGGAT
 618 Y  D  E  V  Y  Q  A  Q  N  Q  Q  P  A  P  V  V  V  K  L  P  T  K  N  E  E  A  R  K  V  V  L  Y  N  S  L  D
1963 TACGACAGAACTGGTGTCGTGCGTCTAATTGTTACGTCACCCGACGTGGTTGTGATGTCAGAAAACAAAAACGTCGTTCCATCGCAAACCAGTCCGATCTGGTCAGATT
 655 Y  D  R  T  G  V  V  R  L  I  V  T  S  P  D  V  V  V  M  S  E  N  K  N  V  V  P  S  Q  T  S  P  I  W  S  D
2072 CGACGGAGATCCGCACAGACCAGTTTGAACTGGTTTTCCTTTCAACTGTTCCCGCGATAGGACTGGCGGTGTACAAGATATGGGAAGACAACGACGTAGCAGACACCAC
 691 S  T  E  I  R  T  D  Q  F  E  L  V  F  L  S  T  V  P  A  I  G  L  A  V  Y  K  I  W  E  D  N  D  V  A  D  T  T
2181 GCACTCAACTGTTAAGTTTATCAACCCGAGAGTTGGGTTTTCGAAACGAACCCGCAGTAAGTTTGTACTCGACGTTGAGGATAGCGGGGAGTTTACCATCATGAATGAC
 727 H  S  T  V  K  F  I  N  P  R  V  G  F  S  K  R  T  R  S  K  F  V  L  D  V  E  D  S  G  E  F  T  I  M  N  D
2290 CAATTAGTTGCGCATTTCTCTGGACAAAACGGGATGCTGCAGTCAGTCACCACTGTGCGTGACAACGTTAAAACGCAGCTCGGAATTGAATTCGTCGCTTATACTTCTC
 764 Q  L  V  A  H  F  S  G  Q  N  G  M  L  Q  S  V  T  T  V  R  D  N  V  K  T  Q  L  G  I  E  F  V  A  Y  T  S
2399 GTAATAAGAAAGACAAGAGCGGCGCTTACTTGTTCCTGCCTGCTGGACCAGCACAACCGCATGTAACAGAATCCCACCGACCGTTAGTAAGGATCATCAGGGGTCCAGT
 800 R  N  K  K  D  K  S  G  A  Y  L  F  L  P  A  G  P  A  Q  P  H  V  T  E  S  H  R  P  L  V  R  I  I  R  G  P  V
2508 GATGTCAACGGTGCATGTTCTACTACCGAACGTTCTGCATAAAGTTACCCTATACACCGGTACTGGTGCAGGCACGCAGTCTTTAGGCGTCCACGTCTCTAACGACGTC
 836 M  S  T  V  H  V  L  L  P  N  V  L  H  K  V  T  L  Y  T  G  T  G  A  G  T  Q  S  L  G  V  H  V  S  N  D  V
2617 GACGTTAGAACTGGCTACGACAACAAAGAACTCAGTATGAGGTTAAACAGCGAAGTTTTATCGGGAAGCAAATTCTTTACGGATTTAAACGGTTTCCAAATTCAACCCC
 873 D  V  R  T  G  Y  D  N  K  E  L  S  M  R  L  N  S  E  V  L  S  G  S  K  F  F  T  D  L  N  G  F  Q  I  Q  P
2726 GAACCACGTATTCTAAACTGCCACTACAAGCAAACTTCTACCCAATACCCACAATGGCGTTCATACAAGACGAAAAATCAAGATTAACTTTGATGACGGCCCAACCACT
 909 R  T  T  Y  S  K  L  P  L  Q  A  N  F  Y  P  I  P  T  M  A  F  I  Q  D  E  K  S  R  L  T  L  M  T  A  Q  P  L
2835 GGGTGTTGCCTCACTGAAGTCAGGTCAACTTGAGGTGGTTTTGGATCGCCGTTTAATGCAGGACGACAACAGGGGGGTGGGTCAAGGTGTGAAAGATAATTTACCAACT
 945 G  V  A  S  L  K  S  G  Q  L  E  V  V  L  D  R  R  L  M  Q  D  D  N  R  G  V  G  Q  G  V  K  D  N  L  P  T
2944 CCTGAGAGTTTCGTGATCATGCTGGAAAGATGGACCGCTATTGCAGCGAAAGAAAGCAAATCGTCAGCGAAGCTCGCGTATCCATCTATGGCTGTGTATCAGTCATCAT
 982 P  E  S  F  V  I  M  L  E  R  W  T  A  I  A  A  K  E  S  K  S  S  A  K  L  A  Y  P  S  M  A  V  Y  Q  S  S
3053 GGGAATTGCTACACCCAATACGTCCAATGTCGGTAAATGGGCCGGTACATTTGAAAGAAGATTACCGCTCGCTGCCACAGCCTTTACCATGCGACGTGCACGTGTTAAA
1018 W  E  L  L  H  P  I  R  P  M  S  V  N  G  P  V  H  L  K  E  D  Y  R  S  L  P  Q  P  L  P  C  D  V  H  V  L  N
3162 CTTGCGAGCAATTCATTCTAAAGATGCAGTTGCCCCTACCGACCAATCGGCTCTGCTTCTACACACAGTTGGGCGCGAATGCTCCTTGGACGCGGATAAGTATTTCCAC
1054 L  R  A  I  H  S  K  D  A  V  A  P  T  D  Q  S  A  L  L  L  H  T  V  G  R  E  C  S  L  D  A  D  K  Y  F  H
3271 CCAACGTGCCTCATGCACGGCGTCGAGAAATTGGCTATCACGATCTCGACGCTTTTTACTAACTCTGGCATGCGGAAGACGTCGCTGTCCTTACAACACGACGGCTCGT
1091 P  T  C  L  M  H  G  V  E  K  L  A  I  T  I  S  T  L  F  T  N  S  G  M  R  K  T  S  L  S  L  Q  H  D  G  S
3380 TGCTGGACAACCAAGGCGGTATTACAGTTTCCCCAATGGAGATACAAGCTTACAAAATAGTACTGACGTAA
1127 L  L  D  N  Q  G  G  I  T  V  S  P  M  E  I  Q  A  Y  K  I  V  L  T
```

FIG. 28

Drosophila mannosidase II (X77652)

```
   1 ATGTTGCGAATACGTCGGCGGTTCGCTTTGGTAATTTGCTCCGGCTGCCTGCTGGTTTTCCTCAGCCTGTACATAATCCTCAATTTTGCGGCGCCGGCAGCCACCCAGA
   1 M  L  R  I  R  R  R  F  A  L  V  I  C  S  G  C  L  L  V  F  L  S  L  Y  I  I  L  N  F  A  A  P  A  A  T  Q
 110 TAAAGCCCAACTATGAGAACATTGAGAACAAGCTGCATGAGCTGGAAAATGGTTTGCAGGAGCACGGGGAGGAGATGCGGAATCTCAGGGCGCGTCTGGCCAAAACATC
  37 I  K  P  N  Y  E  N  I  E  N  K  L  H  E  L  E  N  G  L  Q  E  H  G  E  E  M  R  N  L  R  A  R  L  A  K  T  S
 219 CAATCGCGACGATCCAATAAGACCTCCACTTAAAGTGGCTCGTTCCCCGAGGCCAGGGCAATGCCAAGATGTGGTCCAAGACGTGCCCAATGTGGATGTACAGATGCTG
  73 N  R  D  D  P  I  R  P  P  L  K  V  A  R  S  P  R  P  G  Q  C  Q  D  V  V  Q  D  V  P  N  V  D  V  Q  M  L
 328 GAGCTATACGATCGCATGTCCTTCAAGGACATAGATGGAGGCGTGTGGAAACAGGGCTGGAACATTAAGTACGATCCACTGAAGTACAACGCCCATCACAAACTAAAAG
 110 E  L  Y  D  R  M  S  F  K  D  I  D  G  G  V  W  K  Q  G  W  N  I  K  Y  D  P  L  K  Y  N  A  H  H  K  L  K
 437 TCTTCGTTGTGCCGCACTCGCACAACGATCCTGGATGGATTCAGACGTTTGAGGAATACTACCAGCACGACACCAAGCACATCCTGTCCAATGCACTACGGCATCTGCA
 146 V  F  V  V  P  H  S  H  N  D  P  G  W  I  Q  T  F  E  E  Y  Y  Q  H  D  T  K  H  I  L  S  N  A  L  R  H  L  H
 546 CGACAATCCCGAGATGAAGTTCATCTGGGCGGAAATCTCCTACTTTGCTCGGTTCTATCACGATTTGGGAGAGAACAAAAAGCTGCAGATGAAGTCCATTGTAAAGAAT
 182 D  N  P  E  M  K  F  I  W  A  E  I  S  Y  F  A  R  F  Y  H  D  L  G  E  N  K  K  L  Q  M  K  S  I  V  K  N
 655 GGACAGTTGGAATTTGTGACTGGAGGATGGGTAATGCCGGACGAGGCCAACTCCCACTGGCGAAACGTACTGCTGCAGCTGACCGAAGGGCAAACATGGTTGAAGCAAT
 219 G  Q  L  E  F  V  T  G  G  W  V  M  P  D  E  A  N  S  H  W  R  N  V  L  L  Q  L  T  E  G  Q  T  W  L  K  Q
 764 TCATGAATGTCACACCCACTGCTTCCTGGGCCATCGATCCCTTCGGACACAGTCCCACTATGCCGTACATTTTGCAGAAGAGTGGTTTCAAGAATATGCTTATCCAAAG
 255 F  M  N  V  T  P  T  A  S  W  A  I  D  P  F  G  H  S  P  T  M  P  Y  I  L  Q  K  S  G  F  K  N  M  L  I  Q  R
 873 GACGCACTATTCGGTTAAGAAGGAACTGGCCCAACAGCGACAGCTTGAGTTCCTGTGGCGCCAGATCTGGGACAACAAAGGGGACACAGCTCTCTTCACCCACATGATG
 291 T  H  Y  S  V  K  K  E  L  A  Q  Q  R  Q  L  E  F  L  W  R  Q  I  W  D  N  K  G  D  T  A  L  F  T  H  M  M
 982 CCCTTCTACTCGTACGACATTCCTCATACCTGTGGTCCAGATCCCAAGGTTTGCTGTCAGTTCGATTTCAAACGAATGGGCTCCTTCGGTTTGAGTTGTCCATGGAAGG
 328 P  F  Y  S  Y  D  I  P  H  T  C  G  P  D  P  K  V  C  C  Q  F  D  F  K  R  M  G  S  F  G  L  S  C  P  W  K
1091 TGCCGCCGCGTACAATCAGTGATCAAAATGTGGCAGCACGCTCAGATCTGCTGGTTGATCAGTGGAAGAAGAAGGCCGAGCTGTATCGCACAAACGTGCTGCTGATTCC
 364 V  P  P  R  T  I  S  D  Q  N  V  A  A  R  S  D  L  L  V  D  Q  W  K  K  K  A  E  L  Y  R  T  N  V  L  L  I  P
1200 GTTGGGTGACGACTTCCGCTTCAAGCAGAACACCGAGTGGGATGTGCAGCGCGTGAACTACGAAAGGCTGTTCGAACACATCAACAGCCAGGCCCACTTCAATGTCCAG
 400 L  G  D  D  F  R  F  K  Q  N  T  E  W  D  V  Q  R  V  N  Y  E  R  L  F  E  H  I  N  S  Q  A  H  F  N  V  Q
1309 GCGCAGTTCGGCACACTGCAGGAATACTTTGATGCAGTGCACCAGGCGGAAAGGGCGGGACAAGCCGAGTTTCCCACGCTAAGCGGTGACTTTTTCACATACGCCGATC
 437 A  Q  F  G  T  L  Q  E  Y  F  D  A  V  H  Q  A  E  R  A  G  Q  A  E  F  P  T  L  S  G  D  F  F  T  Y  A  D
1418 GATCGGATAACTATTGGAGTGGCTACTACACATCCCGCCCGTATCATAAGCGCATGGACCGCGTCCTGATGCACTATGTACGTGCAGCAGAAATGCTTTCCGCCTGGCA
 473 R  S  D  N  Y  W  S  G  Y  Y  T  S  R  P  Y  H  K  R  M  D  R  V  L  M  H  Y  V  R  A  A  E  M  L  S  A  W  H
1527 CTCCTGGGACGGTATGGCCCGCATCGAGGAACGTCTGGAGCAGGCCCGCAGGGAGCTGTCATTGTTCCAGCACCACGACGGTATAACTGGCACAGCAAAAACGCACGTA
 509 S  W  D  G  M  A  R  I  E  E  R  L  E  Q  A  R  R  E  L  S  L  F  Q  H  H  D  G  I  T  G  T  A  K  T  H  V
1636 GTCGTCGACTACGAGCAACGCATGCAGGAAGCTTTAAAAGCCTGTCAAATGGTAATGCAACAGTCGGTCTACCGATTGCTGACAAAGCCCTCCATCTACAGTCCGGACT
 546 V  V  D  Y  E  Q  R  M  Q  E  A  L  K  A  C  Q  M  V  M  Q  Q  S  V  Y  R  L  L  T  K  P  S  I  Y  S  P  D
1745 TCAGTTTCTCGTACTTTACGCTCGACGACTCCCGCTGGCCAGGATCTGGTGTGGAGGACAGTCGAACCACCATAATACTGGGCGAGGATATACTGCCCTCCAAGCATGT
 582 F  S  F  S  Y  F  T  L  D  D  S  R  W  P  G  S  G  V  E  D  S  R  T  T  I  I  L  G  E  D  I  L  P  S  K  H  V
1854 GGTGATGCACAACACCCTGCCCCACTGGCGGGAGCAGCTGGTGGACTTTTATGTATCCAGTCCGTTTGTAAGCGTTACCGACTTGGCAAACAATCCGGTGGAGGCTCAG
 618 V  M  H  N  T  L  P  H  W  R  E  Q  L  V  D  F  Y  Y  V  S  S  P  F  V  S  V  T  D  L  A  N  N  P  V  E  A  Q
1963 GTGTCCCCGGTGTGGAGCTGGCACCACGACACACTCACAAAGACTATCCACCCACAAGGCTCCACCACCAAGTACCGCATCATCTTCAAGGCTCGGGTGCCGCCCATGG
 655 V  S  P  V  W  S  W  H  H  D  T  L  T  K  T  I  H  P  Q  G  S  T  T  K  Y  R  I  I  F  K  A  R  V  P  P  M
2072 GCTTGGCCACCTACGTTTTAACCATCTCCGATTCCAAGCCAGAGCACACCTCGTATGCATCGAATCTCTTGCTCCGTAAAAACCCGACTTCGTTACCATTGGGCCAATA
 691 G  L  A  T  Y  Y  L  T  I  S  D  S  K  P  E  H  T  S  Y  A  S  N  L  L  L  R  K  N  P  T  S  L  P  L  G  Q  Y
2181 TCCGGAGGATGTGAAGTTTGGCGATCCTCGAGATCTCATTGCGGGTTGGTAACGGACCCACCTTGGCCTTTTCGGAGCAGGGTCTCCTTAAGTCCATTCAGCTTACT
 727 P  E  D  V  K  F  G  D  P  R  E  I  S  L  R  V  G  N  G  P  T  L  A  F  S  E  Q  G  L  L  K  S  I  Q  L  T
2290 CAGGATAGCCCACATGTACCGGTGCACTTCAAGTTCCTCAAGTATGGCGTTCGATCGCATGGCGATAGATCCGGTGCCTATCTGTTCCTGCCCAATGGACCAGCTTCGC
 764 Q  D  S  P  H  V  P  V  H  F  K  F  L  K  Y  G  V  R  S  H  G  D  R  S  G  A  Y  L  F  L  P  N  G  P  A  S
2399 CAGTCGAGCTTGGCCAGCCAGTGGTCCTGGTGACTAAGGGCAAACTGGAGTCGTCCGTGAGCGTGGGACTTCCGAGCGTGGTGCACCAGACGATAATGCGCGGTGGTGC
 800 P  V  E  L  G  Q  P  V  V  L  V  T  K  G  K  L  E  S  S  V  S  V  G  L  P  S  V  V  H  Q  T  I  M  R  G  G  A
2508 ACCTGAGATTCGCAATCTGGTGGATATAGGCTCACTGGACAACACGGAGATCGTGATGCGCTTGGAGACGCATATCGACAGCGGCGATATCTTCTACACGGATCTCAAT
 836 P  E  I  R  N  L  V  D  I  G  S  L  D  N  T  E  I  V  M  R  L  E  T  H  I  D  S  G  D  I  F  Y  T  D  L  N
2617 GGATTGCAATTTATCAAGAGGCGGCGTTTGGACAAATTACCTTTGCAGGCCAACTATTATCCCATACCTTCTGGTATGTTCATTGAGGATGCCAATACGCGACTCACTC
 873 G  L  Q  F  I  K  R  R  R  L  D  K  L  P  L  Q  A  N  Y  Y  P  I  P  S  G  M  F  I  E  D  A  N  T  R  L  T
2726 TCCTCACGGGTCAACCGCTGGGTGGATCTTCTCTGGCCTCGGGCGAGCTAGAGATTATGCAAGATCGTCGCCTGGCCAGCGATGATGAACGCGGCCTGGGACAGGGTGT
 909 L  L  T  G  Q  P  L  G  G  S  S  L  A  S  G  E  L  E  I  M  Q  D  R  R  L  A  S  D  D  E  R  G  L  G  Q  G  V
2835 TTTGGACAACAAGCCGGTGCTGCATATTTATCGGCTGGTGCTGGAGAAGGTTAACAACTGTGTCCGACCGTCAAAGCTTCATCCTGCCGGCTATTTGACAAGTGCCGCA
 945 L  D  N  K  P  V  L  H  I  Y  R  L  V  L  E  K  V  N  N  C  V  R  P  S  K  L  H  P  A  G  Y  L  T  S  A  A
2944 CACAAAGCATCGCAGTCACTGCTGGATCCACTGGACAAGTTTATATTCGCTGAAAATGAGTGGATCGGGGCACAGGGGCAATTTGGTGGCGATCATCCTTCGGCTCGTG
 982 H  K  A  S  Q  S  L  L  D  P  L  D  K  F  I  F  A  E  N  E  W  I  G  A  Q  G  Q  F  G  G  D  H  P  S  A  R
3053 AGGATCTCGATGTGTCGGTGATGAGACGCTTAACCAAGAGCTCGGCCAAAACCCAGCGAGTAGGCTACGTTCTGCACCGCACCAATCTGATGCAATGCGGCACTCCAGA
1018 E  D  L  D  V  S  V  M  R  R  L  T  K  S  S  A  K  T  Q  R  V  G  Y  V  L  H  R  T  N  L  M  Q  C  G  T  P  E
3162 GGAGCATACACAGAAGCTGGATGTGTGCCACCTACTGCCGAATGTGGCGAGATGCGAGCGCACGACGCTGACTTTCCTGCAGAATTTGGAGCACTTGGATGGCATGGTG
1054 E  H  T  Q  K  L  D  V  C  H  L  L  P  N  V  A  R  C  E  R  T  T  L  T  F  L  Q  N  L  E  H  L  D  G  M  V
3271 GCGCCGGAAGTGTGCCCCATGGAAACCGCCGCTTATGTGAGCAGTCACTCAAGCTGA
1091 A  P  E  V  C  P  M  E  T  A  A  Y  V  S  S  H  S  S
```

FIG. 29

Human mannosidase II (U31520)

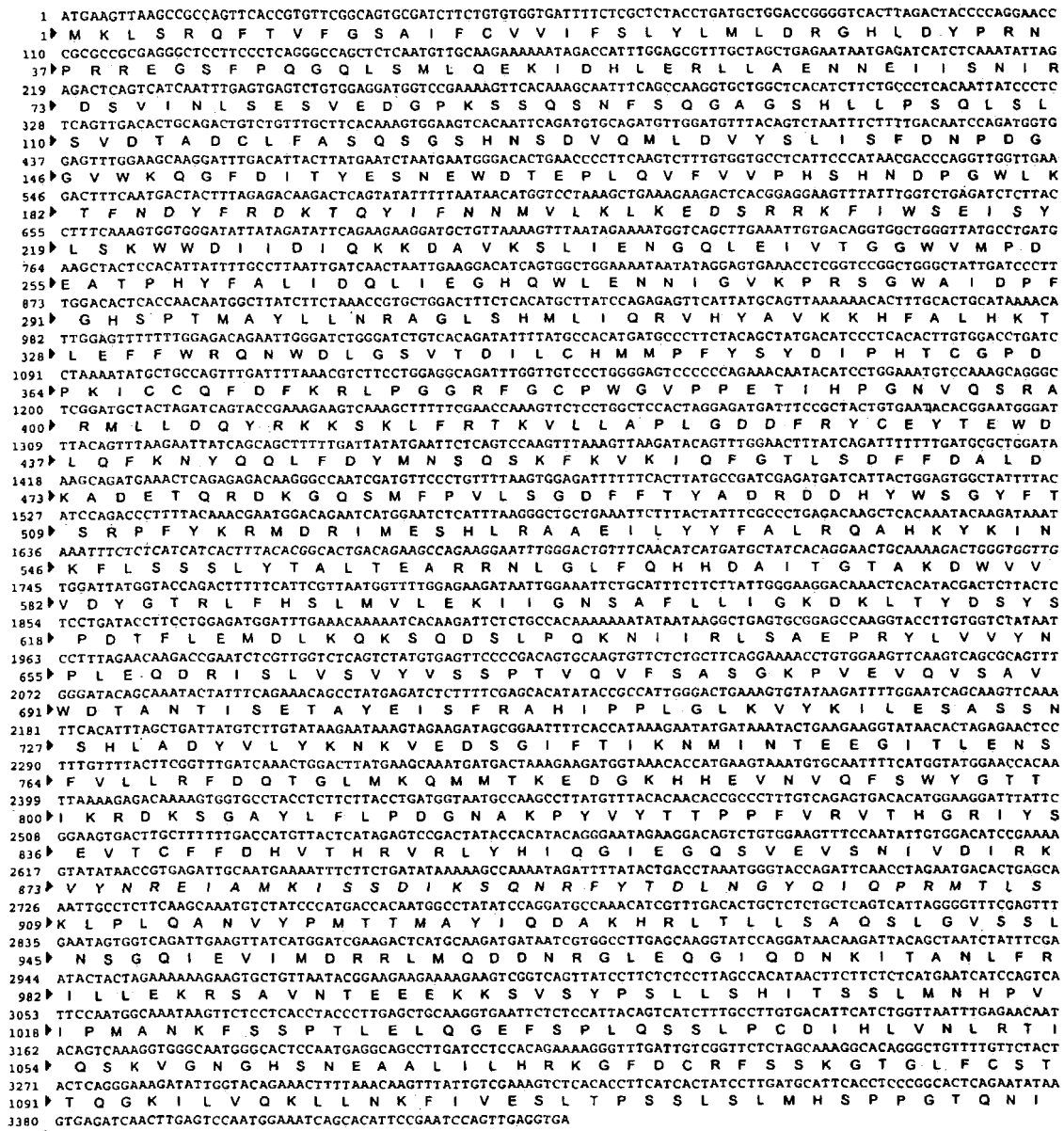

FIG. 30

Mouse mannosidase II (X61172)

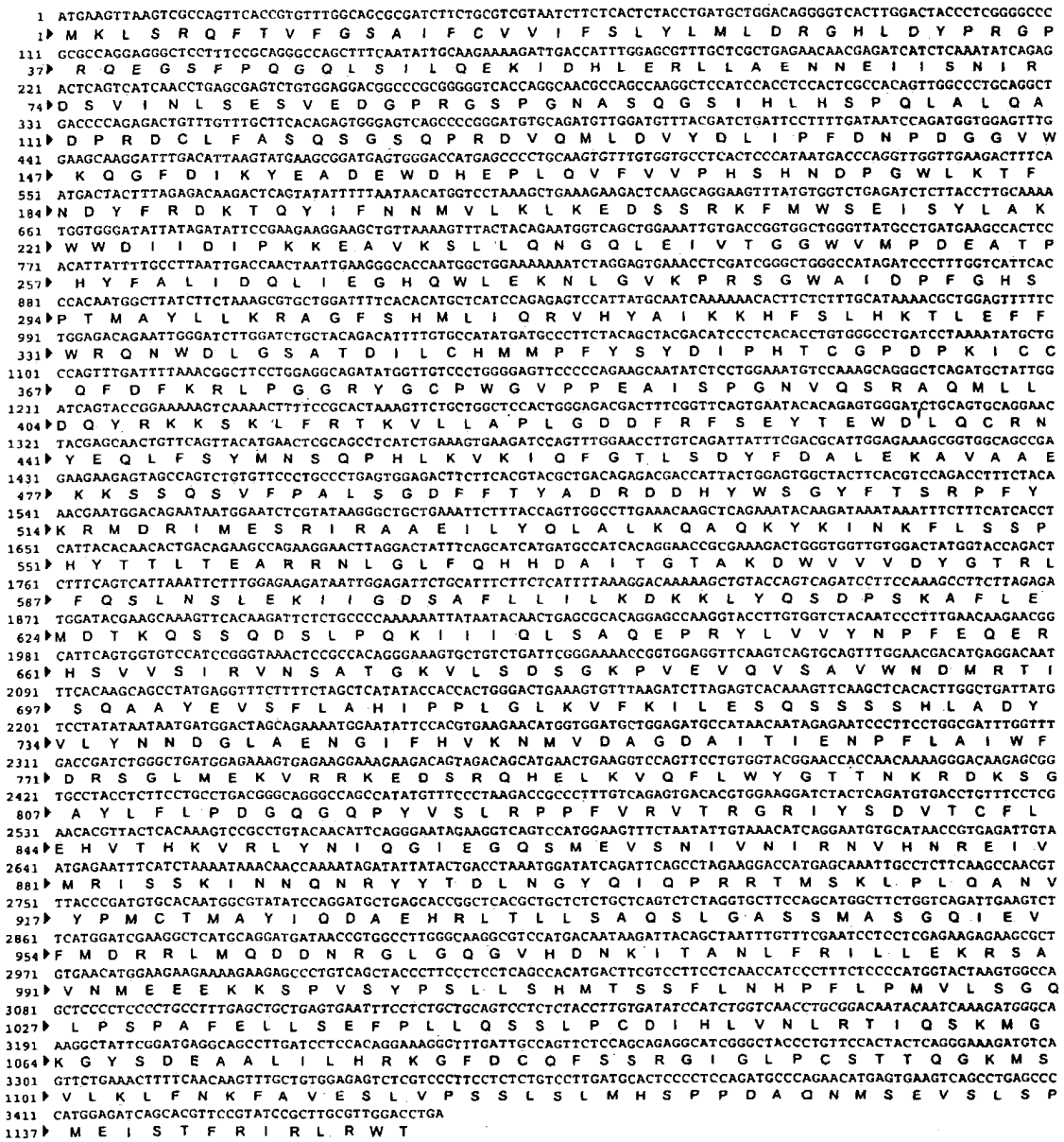

FIG. 31

Rat mannosidase II (XM_218816)

```
   1 ATGGCCTGTATAGGTGGAGCCCAGGGGCAACGGCAGGCCGTGGAAAAGGAACCTTCCCACCAAGGGTATCCGTGGAAGCCAATGACCAATGGCAGCTGCTCAGAACTG
   1 M  A  C  I  G  G  A  Q  G  Q  R  Q  A  V  E  K  E  P  S  H  Q  G  Y  P  W  K  P  M  T  N  G  S  C  S  E  L
 109 GCATTGCTCAGCAAAACCCGAATGTACTGTCACCAGGGATGTGTCAGGCCACCCAGGACTGACGTGAAAAACTTCAAGACCACAACTGATACTCAGAGTGTGCCTGGT
  37 A  L  L  S  K  T  R  M  Y  C  H  Q  G  C  V  R  P  P  R  T  D  V  K  N  F  K  T  T  T  D  T  Q  S  V  P  G
 217 GTCAGTATGAAGCTGAAAAAGCAGGTGACAGTGTGCGGGGCTGCTATCTTCTGTGTGGCCGTCTTTTCCCTGTACCTAATGCTGGACCGAGTGCAGCATGATCCTGCC
  73 V  S  M  K  L  K  K  Q  V  T  V  C  G  A  A  I  F  C  V  A  V  F  S  L  Y  L  M  L  D  R  V  Q  H  D  P  A
 325 AGACACCAGAATGGTGGGAACTTCCCCAGGAGCCAAATTTCTGTGCTACAGAACCGGATCGAACAGCTGGAACAGCTGCTGGAAGAAAACCATGAGATCATAAGCCAT
 109 R  H  Q  N  G  G  N  F  P  R  S  Q  I  S  V  L  Q  N  R  I  E  Q  L  E  Q  L  L  E  E  N  H  E  I  I  S  H
 433 ATCAAGGACTCTGTGCTGGAACTGACAGCCAATGCGGAGGGCCCACCAGCCCTGCTGCCCTACCACACAGCCAACGGCTCCTGGGCTGTGCTCCCCGAGCCCCGGCCC
 145 I  K  D  S  V  L  E  L  T  A  N  A  E  G  P  P  A  L  L  P  Y  H  T  A  N  G  S  W  A  V  L  P  E  P  R  P
 541 AGCTTCTTCTCTGTATCCCCTGAGGACTGCCAGTTTGCTTTGGGGGGCCGGGGTCAGAAGCCAGAGCTACAGATGTTAACTGTGTCTGAGGATTTGCCGTTTGACAAT
 181 S  F  F  S  V  S  P  E  D  C  Q  F  A  L  G  G  R  G  Q  K  P  E  L  Q  M  L  T  V  S  E  D  L  P  F  D  N
 649 GTGGAGGGCGGCGTGTGGAGGCAAGGCTTCGACATCTCCTACAGCCCAAATGACTGGGATGCTGAAGACCTGCAGGTGTTTGTGGTGCCTCACTCCCACAATGATCCA
 217 V  E  G  G  V  W  R  Q  G  F  D  I  S  Y  S  P  N  D  W  D  A  E  D  L  Q  V  F  V  V  P  H  S  H  N  D  P
 757 GGTGAAGAGCCAGCAGGCCCCAGCCGCAGCGTGCAGGGTGGGCTTTCTGGTGACAGGCGCTGGATCAAGACTTTTGACAAGTACTACACGGAACAAACCCAACACATC
 253 G  E  E  P  A  G  P  S  R  S  V  Q  G  G  L  S  G  D  R  R  W  I  K  T  F  D  K  Y  Y  T  E  Q  T  Q  H  I
 865 CTCAACAGCATGGTGTCCAAGCTGCAGGAAGATCCCCGACGGCGCTTTCTCTGGGCAGAAGTCTCCTTCTTCGCCAAGTGGTGGGACAACATCAGTGCCCAGAAAAGG
 289 L  N  S  M  V  S  K  L  Q  E  D  P  R  R  R  F  L  W  A  E  V  S  F  F  A  K  W  W  D  N  I  S  A  Q  K  R
 973 GCAGCAGTTCGAAGGCTGGTGGGAAATGGGCAGCTGGAAATTGCAACGGGTGGATGGGTGATGCCAGATGAGGCCAACTCCCATTACTTTGCCCTGGTGGGGCAGCTC
 325 A  A  V  R  R  L  V  G  N  G  Q  L  E  I  A  T  G  G  W  V  M  P  D  E  A  N  S  H  Y  F  A  L  V  G  Q  L
1081 ATCGAGGGGCCCCCCCCGGTACGCAGGGCAGTGGACCCCTTTGGACACAGCTCCACCATGCCTTACCTGCTGCGCCGTGCCAACCTGACCAGCATGCTAATTCAGAGG
 361 I  E  G  P  P  P  V  R  R  A  V  D  P  F  G  H  S  S  T  M  P  Y  L  L  R  R  A  N  L  T  S  M  L  I  Q  R
1189 GTGCATTACGCCATCAAGAAGCACTTTGCGGCCACTCACAGCCTGGAGTTCATGTGGAGGCAGACATGGGATTCAGACTCCAGCACAGACATCTTCTGCCACATGATG
 397 V  H  Y  A  I  K  K  H  F  A  A  T  H  S  L  E  F  M  W  R  Q  T  W  D  S  D  S  S  T  D  I  F  C  H  M  M
1297 CCCTTCTACAGCTACGACGTCCCACACACCTGTGGCCCTGATCCCAAGATCTGCTGCCAGTTTGATTTCAAACGTCTGCCGGGTGGGAGAATCAATTGTCCTTGGAAG
 433 P  F  Y  S  Y  D  V  P  H  T  C  G  P  D  P  K  I  C  C  Q  F  D  F  K  R  L  P  G  G  R  I  N  C  P  W  K
1405 GTGCCGCCGCGGGCTATCACAGAGGCCAACGTGGCAGACAGGGCAGCCCTGCTCCTGGACCAGTACCGGAAGAAGTCCCGGCTGTTTCGAAGCAGTGTCCTCCTTGTG
 469 V  P  P  R  A  I  T  E  A  N  V  A  D  R  A  A  L  L  L  D  Q  Y  R  K  K  S  R  L  F  R  S  S  V  L  L  V
1513 CCGCTGGGTGATGACTTCCGATATGACAAGCCCCAGGAATGGGATGCCCAGTTCTTCAACTATCAACGGCTCTTTGACTTCCTCAACAGCAAGCCGGAGTTCCACGTA
 505 P  L  G  D  D  F  R  Y  D  K  P  Q  E  W  D  A  Q  F  F  N  Y  Q  R  L  F  D  F  L  N  S  K  P  E  F  H  V
1621 CAGGCACAGTTTGGGACCCTCTCTGAGTATTTTGATGCCCTGTATAAGAGGACAGGAGTGGAGCCTGGTGCCCGGCCTCCAGGGTTTCCTGTGCTGAGTGGGGACTTC
 541 Q  A  Q  F  G  T  L  S  E  Y  F  D  A  L  Y  K  R  T  G  V  E  P  G  A  R  P  P  G  F  P  V  L  S  G  D  F
1729 TTCTCCTATGCTGACCGGGAGGACCACTACTGGACAGGCTATTACACTTCCCGGCCTTTCTATAAGAGCTTGGACCGCGTGCTAGAAACTCACCTTCGTGGGGCAGAG
 577 F  S  Y  A  D  R  E  D  H  Y  W  T  G  Y  Y  T  S  R  P  F  Y  K  S  L  D  R  V  L  E  T  H  L  R  G  A  E
1837 GTTCTATACAGCCTGGCTTTGGCGCATGCCCGCCGTTCTGGACTGACTGGCCAGTATCCGCTGTCTGATTACGCTGTCCTGACGGAAGCTCGTCGTACACTGGGCCTC
 613 V  L  Y  S  L  A  L  A  H  A  R  R  S  G  L  T  G  Q  Y  P  L  S  D  Y  A  V  L  T  E  A  R  R  T  L  G  L
1945 TTCCAGCACCACGATGCCATCACCGGAACTGCCAAGGAGGCAGTTGTAGTAGACTATGGGGTCAGGTTGCTGCGTTCCCTGGTCAGCCTAAAGCAGGTCATCATCAAT
 649 F  Q  H  H  D  A  I  T  G  T  A  K  E  A  V  V  V  D  Y  G  V  R  L  L  R  S  L  V  S  L  K  Q  V  I  I  N
2053 GCTGCCCACTACCTGGTGCTGGGGGACAAGGAGACCTACAGCTTTGACCCTAGGGCACCCTTCCTCCAAATGGTGAGCCAGGCCTGGCGAGGCTCTCAGAGCACCCTC
 685 A  A  H  Y  L  V  L  G  D  K  E  T  Y  S  F  D  P  R  A  P  F  L  Q  M  V  S  Q  A  W  R  G  S  Q  S  T  L
2161 CACCCCAGCGCGGGCCCTTGTTCCTGCTGCTGCTGCTTCTGCCCTGCTGCCGCAGCGAGCTCCTAGGTTTGTGGTGGTCTTTAACCCACTGGAACAGGAGCGGCTCAGT
 721 H  P  S  A  A  L  V  P  A  A  A  A  S  A  L  L  P  Q  R  A  P  R  F  V  V  V  F  N  P  L  E  Q  E  R  L  S
2269 GTGGTGTCCCTGCTGGTCAACTCACCCCGAGTGCGAGTGCTTTCAGAGGAGGGTCAGCCCTTGTCTGTGCAGATCAGTGTGCAGTGGAGCTCCGCCACCAACATGGTC
 757 V  V  S  L  L  V  N  S  P  R  V  R  V  L  S  E  E  G  Q  P  L  S  V  Q  I  S  V  Q  W  S  S  A  T  N  M  V
2377 CCCGATGTCTACCAGGTGTCAGTGCCTGTCCGCCTGCCAGCCCTGGGCCTGGGTGTGCTGCAGCTGCAGCCAGATCTCGATGGACCCTACACACTGCAGTCTTCGGTG
 793 P  D  V  Y  Q  V  S  V  P  V  R  L  P  A  L  G  L  G  V  L  Q  L  Q  P  D  L  D  G  P  Y  T  L  Q  S  S  V
2485 CATGTCTACCTGAACGGCGTGAAACTGTCTGTCAGCAGGCAAACAACATTCCCTCTCCGTGTTGTGGACTCGGGCACCAGTGACTTCGCCATCAGCAATCGATACATG
 829 H  V  Y  L  N  G  V  K  L  S  V  S  R  Q  T  T  F  P  L  R  V  V  D  S  G  T  S  D  F  A  I  S  N  R  Y  M
2593 CAGGTCTGGTTCTCCGGCCTTACTGGGCTTCTCAAGAGCGTCCGACGTGTGGACGAAGAGCAGGAACAGCAGGTGGACATGAAGCTCTTCGTCTATGGAACCCGCACA
 865 Q  V  W  F  S  G  L  T  G  L  L  K  S  V  R  R  V  D  E  E  Q  E  Q  Q  V  D  M  K  L  F  V  Y  G  T  R  T
2701 TCCAAGGATAAGAGTGGTGCCTACCTCTTCCTGCCTGATAACGAGGCTAAGCCCTATGTCCCTAAGAAACCTCCTGTGCTGCGCGTCACCGAAGGCCCTTTCTTCTCA
 901 S  K  D  K  S  G  A  Y  L  F  L  P  D  N  E  A  K  P  Y  V  P  K  K  P  P  V  L  R  V  T  E  G  P  F  F  S
2809 GAGGTGGCTGCGTATTATGAGCACTTTCACCAAGTGATTCGACTTTACAACCTGCCAGGGGTAGAGGGGCTGTCTCTGGACGTGTCGTTCCAGGTGGACATCAGGGAC
 937 E  V  A  A  Y  Y  E  H  F  H  Q  V  I  R  L  Y  N  L  P  G  V  E  G  L  S  L  D  V  S  F  Q  V  D  I  R  D
2917 TACGTGAACAAGGAGCTAGCCCTGCGCATCCACACAGACATCGACAGCCAGGGCACTTTCTTCACAGACCTCAATGGCTTTCAGGTACAGCCCCGGAAGTATCTGAAG
 973 Y  V  N  K  E  L  A  L  R  I  H  T  D  I  D  S  Q  G  T  F  F  T  D  L  N  G  F  Q  V  Q  P  R  K  Y  L  K
3025 AAGTTGCCCCTGCAGGCTAATTTCTACCCTATGCCAGTCATGGCCTACATCCAGGATTCCCAGAGGCGCCTCACGCTGCACACTGCTCAGGCTCTGGGTGTCTCCAGC
1009 K  L  P  L  Q  A  N  F  Y  P  M  P  V  M  A  Y  I  Q  D  S  Q  R  R  L  T  L  H  T  A  Q  A  L  G  V  S  S
3133 CTCGGCAATGGCCAGCTGGAGGTGATCTTGGACCGAAGGCTAATGCAGGATGACAACCGGGGACTAGGCCAAGGGCTCAAAGACAACAAGATCACCTGCAACCATTTC
1045 L  G  N  G  Q  L  E  V  I  L  D  R  R  L  M  Q  D  D  N  R  G  L  G  Q  G  L  K  D  N  K  I  T  C  N  H  F
3241 CGCCTCCTGTTAGAACGTCGAACCCTGATGAGCCCTGAGGTCCAACAGGAGCGCTCTACAAGCTACCCGTCCCTCCTCAGCCACATGACTTCCATGTACCTCAACACA
1081 R  L  L  L  E  R  R  T  L  M  S  P  E  V  Q  Q  E  R  S  T  S  Y  P  S  L  L  S  H  M  T  S  M  Y  L  N  T
3349 CCTCCTCTGGTCTTACCGGTGGCCAAGAGGGAGAGCACCAGCCCCACTCTGCACTCTTTCCACCCTCTGGCTTCTCCGTTGCCCTGCGATTTCCATCTGCTCAATCTG
1117 P  P  L  V  L  P  V  A  K  R  E  S  T  S  P  T  L  H  S  F  H  P  L  A  S  P  L  P  C  D  F  H  L  L  N  L
3457 CGCATGCTCCCCCGCCGAGGTGAGTGTCCCGGTCCGTGCCAATCCTCACCATCAGGCTGAGCCTTGCCTTCTTGGCAGACATGCTGCTGACCCTCCACCGCTCTTGTCC
1153 R  M  L  P  A  E  V  S  V  P  V  R  A  N  P  H  H  Q  A  E  P  C  L  L  G  R  H  A  A  D  P  P  P  L  L  S
3565 CTGACTGTCTTCCAGGACACCTTGCCCGCGGCTGATGCTGCTCTCATCCTACACCGCAAGGGTTTTGACTGTGGCCTTGAAGCCAAGAACCTGGGCTTCAACTGTACC
1189 L  T  V  F  Q  D  T  L  P  A  A  D  A  A  L  I  L  H  R  K  G  F  D  C  G  L  E  A  K  N  L  G  F  N  C  T
3673 ACAAGCCAAGGCAAGCTGGCCCTGGGGAGCCTCTTCCATGGCCTGGATGTGCTATTCCTGCAGCCCACCTCTTTGACTTTGCTATACCCTCTGGCCTCGCCCTCCAAC
1225 T  S  Q  G  K  L  A  L  G  S  L  F  H  G  L  D  V  L  F  L  Q  P  T  S  L  T  L  L  Y  P  L  A  S  P  S  N
3781 AGCACTGACATCTCTCTGGAGCCCATGGAGATCAGCACCTTCCGCCTGCGCTTGGGTTAG
1261 S  T  D  I  S  L  E  P  M  E  I  S  T  F  R  L  R  L  G
```

FIG. 32

Human mannosidase IIx (D55649)

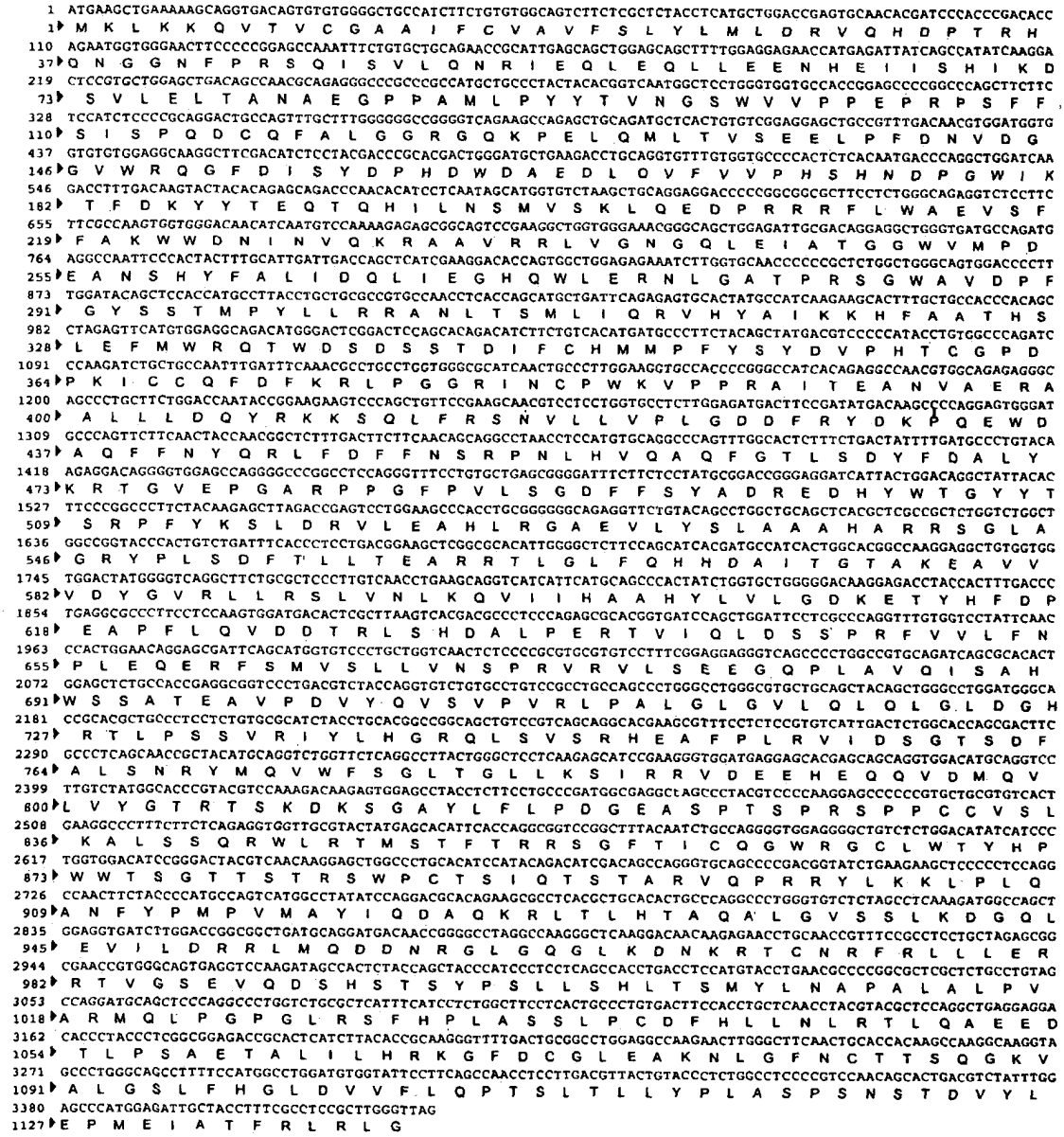

FIG. 33

Insect cell mannosidase III (AF005034)

```
   1 ATGAGGACTCGTGTCCTTCGTTGCCGGCCGTTCTCCACCCGGATCCTGCTGCTGCTGCTATTTGTCCTTGCGTTTGGGGTCTACTGCTATTTCTACAATGCATCTCCTCA
   1 M  R  T  R  V  L  R  C  R  P  F  S  T  R  I  L  L  L  L  L  F  V  L  A  F  G  V  Y  C  Y  F  Y  N  A  S  P  Q
 111 GAACTATAACAAACCAAGAATCAGTTACCCAGCCAGTATGGAGCACTTCAAATCTTCCCTCACTCACACCGTCAAGAGCCGAGACGAGCCAACTCCGGATCAATGCCCTG
  37 N  Y  N  K  P  R  I  S  Y  P  A  S  M  E  H  F  K  S  S  L  T  H  T  V  K  S  R  D  E  P  T  P  D  Q  C  P
 221 CATTGAAGGAAAGCGAAGCGGACATCGACACCGTGGCGATATACCCAACTTTGATTTTCAGCCGAGCTGGTTGCGTACAAAGGAATTTTGGGACAAGTCCTTCGAGGAT
  74 A  L  K  E  S  E  A  D  I  D  T  V  A  I  Y  P  T  F  D  F  Q  P  S  W  L  R  T  K  E  F  W  D  K  S  F  E  D
 331 CGGTATGAAAGAATTCATAACGACACTACACGGCCTAGACTGAAGGTAATCGTGGTTCCTCACTCACACAACGACCCGGGATGGCTGAAGACGTTTGAACAGTACTTCGA
 111 R  Y  E  R  I  H  N  D  T  T  R  P  R  L  K  V  I  V  V  P  H  S  H  N  D  P  G  W  L  K  T  F  E  Q  Y  F  E
 441 GTGGAAGACCAAGAACATTATCAACAACATAGTGAACAAACTGCACCAGTACCCCAACATGACCTTCATTTGGACCGAGATATCGTTTCTGAATGCCTGGTGGGAAAGGT
 147 W  K  T  K  N  I  I  N  N  I  V  N  K  L  H  Q  Y  P  N  M  T  F  I  W  T  E  I  S  F  L  N  A  W  W  E  R
 551 CGCACCCTGTCAAACAAAAGGCATTGAAAAAACTTATCAAAGAAGGTCGTCTCGAGATCACGACGGGCGGCTGGGTGATGCCGGACGAAGCCTGCACGCATATCTATGCG
 184 S  H  P  V  K  Q  K  A  L  K  K  L  I  K  E  G  R  L  E  I  T  T  G  G  W  V  M  P  D  E  A  C  T  H  I  Y  A
 661 CTAATTGACCAGTTTATTGAAGGACATCACTGGGTGAAAACTAATCTCGGCGTCATCCCGAAGACAGGATGGTCTATTGACCCCTTCGGCCACGGGGCCACTGTGCCTTA
 221 L  I  D  Q  F  I  E  G  H  H  W  V  K  T  N  L  G  V  I  P  K  T  G  W  S  I  D  P  F  G  H  G  A  T  V  P  Y
 771 CCTGCTAGACCAGAGCGGCCTTGAGGGAACCATTATACAGAGAATCCATTATGCGTGGAAACAGTGGCTGGCGGAGCGACAGATTGAGGAGTTTTACTGGCTGGCGAGTT
 257 L  L  D  Q  S  G  L  E  G  T  I  I  Q  R  I  H  Y  A  W  K  Q  W  L  A  E  R  Q  I  E  E  F  Y  W  L  A  S
 881 GGGCTACTACGAAGCCGTCCATGATAGTGCACAATCAGCCGTTTGATATTTATTCAATAAAAAGCACGTGTGGCCCGCACCCTTCAATTTGTCTCAGTTTCGACTTCAGG
 294 W  A  T  T  K  P  S  M  I  V  H  N  Q  P  F  D  I  Y  S  I  K  S  T  C  G  P  H  P  S  I  C  L  S  F  D  F  R
 991 AAGATTCCCGGCGAATATTCTGAATACACAGCTAAGCACGAAGACATCACGGAACACAACTTGCACAGCAAGGCAAAGACTTTGATAGAGGAGTACGACCGTATCGGGTC
 331 K  I  P  G  E  Y  S  E  Y  T  A  K  H  E  D  I  T  E  H  N  L  H  S  K  A  K  T  L  I  E  E  Y  D  R  I  G  S
1101 CCTGACTCCACACAACGTGGTGCTGGTGCCGCTCGGAGACGACTTCAGATACGAGTACAGCGTCGAGTTTGATGCCCAATACGTCAATTATATGAAAATGTTTAACTACA
 367 L  T  P  H  N  V  V  L  V  P  L  G  D  D  F  R  Y  E  Y  S  V  E  F  D  A  Q  Y  V  N  Y  M  K  M  F  N  Y
1211 TCAATGCTCACAAGGAAATCTTCAACGCTGACGTACAGTTCGGAACTCCTCTCGATTACTTTAACGCCATGAAAGAAAGACATCAAAATATACCCAGCTTAAAGGGAGAT
 404 I  N  A  H  K  E  I  F  N  A  D  V  Q  F  G  T  P  L  D  Y  F  N  A  M  K  E  R  H  Q  N  I  P  S  L  K  G  D
1321 TTCTTCGTTTACTCCGATATTTTCAGCGAAGGTAAACCAGCGTACTGGTCAGGTTACTACACTACTAGACCCTACCAAAAAATCCTCGCCCGTCAGTTCGAACACCAACT
 441 F  F  V  Y  S  D  I  F  S  E  G  K  P  A  Y  W  S  G  Y  Y  T  T  R  P  Y  Q  K  I  L  A  R  Q  F  E  H  Q  L
1431 GCGATCGGCAGAGATTTTATTCACCCTTGTATCGAACTACATCAGACAGATGGGTCGCCAAGGAGAGTTCGGAGCTTCTGAGAAAAAGTTAGAAAAATCTTACGAGCAGC
 477 R  S  A  E  I  L  F  T  L  V  S  N  Y  I  R  Q  M  G  R  Q  G  E  F  G  A  S  E  K  K  L  E  K  S  Y  E  Q
1541 TTATCTATGCTCGACGGAACTTGGGTCTGTTTCAACATCACGATGCGATTACTGGAACATCAAAGTCCAGTGTGATGCAAGATTACGGAACCAAACTGTTCACAAGTCTG
 514 L  I  Y  A  R  R  N  L  G  L  F  Q  H  H  D  A  I  T  G  T  S  K  S  S  V  M  Q  D  Y  G  T  K  L  F  T  S  L
1651 TATCACTGCATCCGCCTGCAGGAGGCCGCGCTCACCACCATCATGTTGCCTGACCAGTCGTTGCACTCGCAGAGCATTATACAAAGCGAGGTTGAGTGGGAAACTTACGG
 551 Y  H  C  I  R  L  Q  E  A  A  L  T  T  I  M  L  P  D  Q  S  L  H  S  Q  S  I  I  Q  S  E  V  E  W  E  T  Y  G
1761 AAAACCGCCCAAGAAGCTGCAAGTGTCCTTCATTGACAAGAAGAAAGTTATACTTTTTAATCCGTTGGCTGAGACTCGAACTGAAGTGGTCACGGTTAGATCCAACACGT
 587 K  P  P  K  K  L  Q  V  S  F  I  D  K  K  K  V  I  L  F  N  P  L  A  E  T  R  T  E  V  V  T  V  R  S  N  T
1871 CCAACATCCGGGTGTACGATACACACAAGAGGAAGCACGTCTTGTATCAGATAATGCCCAGCATCACAATCCAAGACAACGGCAAGAGTATCGTAAGCGACACCACGTTC
 624 S  N  I  R  V  Y  D  T  H  K  R  K  H  V  L  Y  Q  I  M  P  S  I  T  I  Q  D  N  G  K  S  I  V  S  D  T  T  F
1981 GACATAATGTTCGTGGCCACCATCCCGCCCCTCACCTCCATCTCGTACAAGCTGCAGGAGCACACCAACACTTCCCACCACTGCGTCATTTTCTGCAACAACTGCGAACA
 661 D  I  M  F  V  A  T  I  P  P  L  T  S  I  S  Y  K  L  Q  E  H  T  N  T  S  H  H  C  V  I  F  C  N  N  C  E  Q
2091 ATACCAGAAATCCAATGTGTTCCAAATTAAGAAAATGATGCCTGGTGACATACAATTAGAAAATGCAGTGCTAAAACTTCTCGTTAATAGGAACACCGGCTTTCTGAGAC
 697 Y  Q  K  S  N  V  F  Q  I  K  K  M  M  P  G  D  I  Q  L  E  N  A  V  L  K  L  L  V  N  R  N  T  G  F  L  R
2201 AAGTCTATAGAAAGGACATCCGGAAGAGAACTGTCGTTGACGTACAATTCGGCGCATATCAAAGTGCCCAAAGACATTCTGGTGCTTACCTCTTCATGCCTCATTACGAC
 734 Q  V  Y  R  K  D  I  R  K  R  T  V  V  D  V  Q  F  G  A  Y  Q  S  A  Q  R  H  S  G  A  Y  L  F  M  P  H  Y  D
2311 TCACCTGAGAAGAATGTTCTGCATCCCTACACTAATCAGAACAACATGCAAGATGATAACATAATCATAGTGTCCGGACCTATTTCTACGGAAATCACGACCATGTACTT
 771 S  P  E  K  N  V  L  H  P  Y  T  N  Q  N  N  M  Q  D  D  N  I  I  I  V  S  G  P  I  S  T  E  I  T  T  M  Y  L
2421 GCCCTTCTTGGTGCACACTATTAGGATATACAACGTGCCGGACCCGGTACTGTCGCGTGCTATTCTATTAGAGACCGATGTAGATTTCGAGGCGCCACCTAAGAACAGAG
 807 P  F  L  V  H  T  I  R  I  Y  N  V  P  D  P  V  L  S  R  A  I  L  L  E  T  D  V  D  F  E  A  P  P  K  N  R
2531 AGACTGAGTTATTTATGACATTACAGACTGATATACAAAACGGTGACATTCCCGAATTTTACACCGATCAGAACGGATTCCAGTACCAAAAGAGGGTCAAAGTGAATAAA
 844 E  T  E  L  F  M  R  L  Q  T  D  I  Q  N  G  D  I  P  E  F  Y  T  D  Q  N  G  F  Q  Y  Q  K  R  V  K  V  N  K
2641 CTAGGAATAGAAGCTAATTACTACCCGATCACTACCATGGCGTGCCTGCAAGACGAGGAGACCCGGCTCACTCTGCTGACGAACCACGCTCAAGGCGCTGCTGCATACGA
 881 L  G  I  E  A  N  Y  Y  P  I  T  T  M  A  C  L  Q  D  E  E  T  R  L  T  L  L  T  N  H  A  Q  G  A  A  A  Y  E
2751 ACCAGGACGCTTAGAAGTCATGCTCGATCGTCGAACTCTTTATGATGACTTCAGAGGAATCGGTGAAGGAGTAGTCGATAACAAACCGACGACTTTCCAGAACTGGATTT
 917 P  G  R  L  E  V  M  L  D  R  R  T  L  Y  D  D  F  R  G  I  G  E  G  V  V  D  N  K  P  T  T  F  Q  N  W  I
2861 TAATTGAATCCATGCCAGGCGTGACGCGAGCCAAGAGAGACACTAGTGAACCAGGTTTCAAATTTGTTAATGAACGTCGTTTTGGCCCCGGCCAGAAGGAAAGCCCTTAC
 954 L  I  E  S  M  P  G  V  T  R  A  K  R  D  T  S  E  P  G  F  K  F  V  N  E  R  R  F  G  P  G  Q  K  E  S  P  Y
2971 CAAGTACCGTCGCAGACTGCGGACTACCTGAGCAGGATGTTCAATTACCCGGTGAACGTGTACCTGGTGGACACTAGCGAGGTTGGCGAGATCGAGGTGAAGCCGTACCA
 991 Q  V  P  S  Q  T  A  D  Y  L  S  R  M  F  N  Y  P  V  N  V  Y  L  V  D  T  S  E  V  G  E  I  E  V  K  P  Y  Q
3081 GTCGTTCCTGCAGAGCTTCCCGCCCGGCATCCACCTGGTCACCCTGCGCACCATCACCGACGACGTGCTCGAACTCTTCCCCAGCAACGAAAGCTACATGGTACTGCACC
1027 S  F  L  Q  S  F  P  P  G  I  H  L  V  T  L  R  T  I  T  D  D  V  L  E  L  F  P  S  N  E  S  Y  M  V  L  H
3191 GACCAGGATACAGCTGCGCTGTCGGAGAGAAGCCAGTCGCCAAGTCTCCCAAGTTTTCGTCCAAAACCAGGTTCAATGGTCTGAACATTCAGAACATCACTGCAGTCAGC
1064 R  P  G  Y  S  C  A  V  G  E  K  P  V  A  K  S  P  K  F  S  S  K  T  R  F  N  G  L  N  I  Q  N  I  T  A  V  S
3301 CTGACCGGCCTGAAGTCACTCCGACCTCTCACAGGTCTGAGTGACATCCACCTGAACGCTATGGAGGTAAAAACTTACAAGATCAGGTTTTAA
1101 L  T  G  L  K  S  L  R  P  L  T  G  L  S  D  I  H  L  N  A  M  E  V  K  T  Y  K  I  R  F
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FIG. 34

Human lysosomal mannosidase II (NM_000528)

```
   1 ATGGGCTACGCGCGGGCTTCGGGGGTCTGCGCTCGCGGCTGCCTGGACTCAGCAGGCCCCTGGACCATGTCCCGCGCCCTGCGGCCACCGCTCCCGCCTCTCTGCTTTT
   1 M  G  Y  A  R  A  S  G  V  C  A  R  G  C  L  D  S  A  G  P  W  T  M  S  R  A  L  R  P  P  L  P  P  L  C  F
 110 TCCTTTTGTTGCTGGCGGCTGCCGGTGCTCGGGCCGGGGGATACGAGACATGCCCCACAGTGCAGCCGAACATGCTGAACGTGCACCTGCTGCCTCACACACATGATGA
  37 F  L  L  L  L  A  A  A  G  A  R  A  G  G  Y  E  T  C  P  T  V  Q  P  N  M  L  N  V  H  L  L  P  H  T  H  D  D
 219 CGTGGGCTGGCTCAAAACCGTGGACCAGTACTTTTATGGAATCAAGAATGACATCCAGCACGCCGGTGTGCAGTACATCCTGGACTCGGTCATCTCTGCCTTGCTGGCA
  73 V  G  W  L  K  T  V  D  Q  Y  F  Y  G  I  K  N  D  I  Q  H  A  G  V  Q  Y  I  L  D  S  V  I  S  A  L  L  A
 328 GATCCCACCCGTCGCTTCATTTACGTGGAGATTGCCTTCTTCTCCCGTTGGTGGCACCAGCAGACAAATGCCACACAGGAAGTCGTGCGAGACCTTGTGCGCCAGGGGC
 110 D  P  T  R  R  F  I  Y  V  E  I  A  F  F  S  R  W  W  H  Q  Q  T  N  A  T  Q  E  V  V  R  D  L  V  R  Q  G
 437 GCCTGGAGTTCGCCAATGGTGGCTGGGTGATGAACGATGAGGCAGCCACCCACTACGGTGCCATCGTGGACCAGATGACACTTGGGCTGCGCTTTCTGGAGGACACATT
 146 R  L  E  F  A  N  G  G  W  V  M  N  D  E  A  A  T  H  Y  G  A  I  V  D  Q  M  T  L  G  L  R  F  L  E  D  T  F
 546 TGGCAATGATGGGCGACCCCGTGTGGCCTGGCACATTGACCCCTTCGGCCACTCTCGGGAGCAGGCCTCGCTGTTTGCGCAGATGGGCTTCGACGGCTTCTTCTTTGGG
 182 G  N  D  G  R  P  R  V  A  W  H  I  D  P  F  G  H  S  R  E  Q  A  S  L  F  A  Q  M  G  F  D  G  F  F  F  G
 655 CGCCTTGATTATCAAGATAAGTGGGTACGGATGCAGAAGCTGGAGATGGAGCAGGTGTGGCGGGCCAGCACCAGCCTGAAGCCCCCGACCGCGGACCTCTTCACTGGTG
 219 R  L  D  Y  Q  D  K  W  V  R  M  Q  K  L  E  M  E  Q  V  W  R  A  S  T  S  L  K  P  P  T  A  D  L  F  T  G
 764 TGCTTCCCAATGGTTACAACCCGCCAAGGAATCTGTGCTGGGATGTGCTGTGTGTCGATCAGCCGCTGGTGGAGGACCCTCGCAGCCCCGAGTACAACGCCAAGGAGCT
 255 V  L  P  N  G  Y  N  P  P  R  N  L  C  W  D  V  L  C  V  D  Q  P  L  V  E  D  P  R  S  P  E  Y  N  A  K  E  L
 873 GGTCGATTACTTCCTAAATGTGGCCACTGCCCAGGGCCGGTATTACCGCACCAACCACACTGTGATGACCATGGGCTCGGACTTCCAATATGAGAATGCCAACATGTGG
 291 V  D  Y  F  L  N  V  A  T  A  Q  G  R  Y  Y  R  T  N  H  T  V  M  T  M  G  S  D  F  Q  Y  E  N  A  N  M  W
 982 TTCAAGAACCTTGACAAGCTCATCCGGCTGGTAAATGCGCAGCAGGCAAAAGGAAGCAGTGTCCATGTTCTCTACTCCACCCCCGCTTGTTACCTCTGGGAGCTGAACA
 328 F  K  N  L  D  K  L  I  R  L  V  N  A  Q  Q  A  K  G  S  S  V  H  V  L  Y  S  T  P  A  C  Y  L  W  E  L  N
1091 AGGCCAACCTCACCTGGTCAGTGAAACATGACGACTTCTTCCCTTACGCGGATGGCCCCCACCAGTTCTGGACCGGTTACTTTTCCAGTCGGCCGGCCCTCAAACGCTA
 364 K  A  N  L  T  W  S  V  K  H  D  D  F  F  P  Y  A  D  G  P  H  Q  F  W  T  G  Y  F  S  S  R  P  A  L  K  R  Y
1200 CGAGCGCCTCAGCTACAACTTCCTGCAGGTGTGCAACCAGCTGGAGGCGCTGGTGGGCCTGGCGGCCAACGTGGGACCCTATGGCTCCGGAGACAGTGCCACCCCTCAAT
 400 E  R  L  S  Y  N  F  L  Q  V  C  N  Q  L  E  A  L  V  G  L  A  A  N  V  G  P  Y  G  S  G  D  S  A  P  L  N
1309 GAGGCGATGGCTGTGCTCCAGCATCACGACGCCGTCAGCGGCACCTCCCGCCAGCACGTGGCCAACGACTACGCGCCCAGCTTGCGGCAGGCTGGGGGCCTTGCGAGG
 437 E  A  M  A  V  L  Q  H  H  D  A  V  S  G  T  S  R  Q  H  V  A  N  D  Y  A  R  Q  L  A  A  G  W  G  P  C  E
1418 TTCTTCTGAGCAACGCGCTGGCGCGGCTCAGAGGCTTCAAAGATCACTTCACCTTTTGCCAACAGCTAAACATCAGCATCTGCCCGCTCAGCCAGACGGCGGCGCGCTT
 473 V  L  L  S  N  A  L  A  R  L  R  G  F  K  D  H  F  T  F  C  Q  Q  L  N  I  S  I  C  P  L  S  Q  T  A  A  R  F
1527 CCAGGTCATCGTTTATAATCCCCTGGGGCGGAAGGTGAATTGGATGGTACGGCTGCCGGTCAGCGAAGGCGTTTTCGTTGTGAAGGACCCCAATGGCAGGACAGTGCCC
 509 Q  V  I  V  Y  N  P  L  G  R  K  V  N  W  M  V  R  L  P  V  S  E  G  V  F  V  V  K  D  P  N  G  R  T  V  P
1636 AGCGATGTGGTAATATTTCCCAGCTCAGACAGCCAGGCGCACCCTCCGGAGCTGCTGTTCTCAGCCTCACTGCCCGCCCTGGGCTTCAGCACCTATTCAGTAGCCCAGG
 546 S  D  V  V  I  F  P  S  S  D  S  Q  A  H  P  P  E  L  L  F  S  A  S  L  P  A  L  G  F  S  T  Y  S  V  A  Q
1745 TGCCTCGCTGGAAGCCCCAGGCCCGCGCACCACAGCCCATCCCCAGAAGATCCTGGTCCCCTGCTTTAACCATCGAAAATGAGCACATCCGGGCAACGTTTGATCCTGA
 582 V  P  R  W  K  P  Q  A  R  A  P  Q  P  I  P  R  R  S  W  S  P  A  L  T  I  E  N  E  H  I  R  A  T  F  D  P  D
1854 CACAGGGCTGTTGATGGAGATTATGAACATGAATCAGCAACTCCTGCTGCCTGTTCGCCAGACCTTCTTCTGGTACAACGCCAGTATAGGTGACAACGAAAGTGACCAG
 618 T  G  L  L  M  E  I  M  N  M  N  Q  Q  L  L  L  P  V  R  Q  T  F  F  W  Y  N  A  S  I  G  D  N  E  S  D  Q
1963 GCCTCAGGTGCCTACATCTTCAGACCCAACCAACAGAAACCGCTGCCTGTGAGCCGCTGGGCTCAGATCCACCTGGTGAAGACACCCTTGGTGCAGGAGGTGCACCAGA
 655 A  S  G  A  Y  I  F  R  P  N  Q  Q  K  P  L  P  V  S  R  W  A  Q  I  H  L  V  K  T  P  L  V  Q  E  V  H  Q
2072 ACTTCTCAGCTTGGTGTTCCCAGGTGGTTCGCCTGTACCCAGGACAGCGGCACCTGGAGCTAGAGTGGTCGGTGGGGCCGATACCTGTGGGCGACACCTGGGGGAAGGA
 691 N  F  S  A  W  C  S  Q  V  V  R  L  Y  P  G  Q  R  H  L  E  L  E  W  S  V  G  P  I  P  V  G  D  T  W  G  K  E
2181 GGTCATCAGCCGTTTTGACACACCGCTGGAGACAAAGGGACGCTTCTACACAGACAGCAATGGCCGGGAGATCCTGGAGAGGAGGCGGGATTATCGACCCACCTGGAAA
 727 V  I  S  R  F  D  T  P  L  E  T  K  G  R  F  Y  T  D  S  N  G  R  E  I  L  E  R  R  R  D  Y  R  P  T  W  K
2290 CTGAACCAGACGGAGCCCGTGGCAGGAAACTACTATCCAGTCAACACCCGGATTTACATCACGGATGGAAACATGCAGCTGACTGTGCTGACTGACCGCTCCCAGGGGG
 764 L  N  Q  T  E  P  V  A  G  N  Y  Y  P  V  N  T  R  I  Y  I  T  D  G  N  M  Q  L  T  V  L  T  D  R  S  Q  G
2399 GCAGCAGCCTGAGAGATGGCTCGCTGGAGCTCATGGTGCACCGAAGGCTGCTGAAGGACGATGGACGCGGAGTATCGGAGCCACTAATGGAGAACGGGTCGGGGGCGTG
 800 G  S  S  L  R  D  G  S  L  E  L  M  V  H  R  R  L  L  K  D  D  G  R  G  V  S  E  P  L  M  E  N  G  S  G  A  W
2508 GGTGCGAGGGCGCCACCTGGTGCTGCTGGACACAGCCCAGGCTGCAGCCGCCGGACACCGGCTCCTGGCGGAGCAGGAGGTCCTGGCCCCTCAGGTGGTGCTGGCCCCG
 836 V  R  G  R  H  L  V  L  L  D  T  A  Q  A  A  A  A  G  H  R  L  L  A  E  Q  E  V  L  A  P  Q  V  V  L  A  P
2617 GGTGGCGGCGCCGCCTACAATCTCGGGGCTCCTCCGCGCACGCAGTTCTCAGGGCTGCGCAGGGACCTGCCGCCCTCGGTGCACCTGCTCACGCTGGCCAGCTGGGGCC
 873 G  G  G  A  A  Y  N  L  G  A  P  P  R  T  Q  F  S  G  L  R  R  D  L  P  P  S  V  H  L  L  T  L  A  S  W  G
2726 CCGAAATGGTGCTGCTGCGCTTGGAGCACCAGTTTGCCGTAGGAGAGGATTCCGGACGTAACCTGAGCGCCCCCGTTACCTTGAACTTGAGGGACCTGTTCTCCACCTT
 909 P  E  M  V  L  L  R  L  E  H  Q  F  A  V  G  E  D  S  G  R  N  L  S  A  P  V  T  L  N  L  R  D  L  F  S  T  F
2835 CACCATCACCCGCCTGCAGGAGACCACGCTGGTGGCCAACCAGCTCCGCGAGGCAGCCTCCAGGCTCAAGTGGACAACAAACACAGGCCCCACACCCCACCAAACTCCG
 945 T  I  T  R  L  Q  E  T  T  L  V  A  N  Q  L  R  E  A  A  S  R  L  K  W  T  T  N  T  G  P  T  P  H  Q  T  P
2944 TACCAGCTGGACCCGGCCAACATCACGCTGGAACCCATGGAAATCCGCACTTTCCTGGCCTCAGTTCAATGGAAGGAGGTGGATGGTTAG
 982 Y  Q  L  D  P  A  N  I  T  L  E  P  M  E  I  R  T  F  L  A  S  V  Q  W  K  E  V  D  G
```

FIG. 35

Human cytoplasmic mannosidase II (NM_006715)

```
   1 ATGGCGGCAGCGCCGTTCTTGAAGCACTGGCGCACCACTTTTGAGCGGGTGGAGAAGTTCGTGTCCCCGATCTACTTCACCGACTGTAACCTCCGCGGCAGGCTTTTTG
   1 M  A  A  A  A  P  F  L  K  H  W  R  T  T  F  E  R  V  E  K  F  V  S  P  I  Y  F  T  D  C  N  L  R  G  R  L  F
 110 GGGCCAGCTGCCCTGTGGCTGTGCTCTCCAGCTTCCTGACGCCGGAGAGACTTCCCTACCAGGAGGCAGTCCAGCGGGACTTCCGCCCCGCGCAGGTCGGCGACAGCTT
  37 G  A  S  C  P  V  A  V  L  S  S  F  L  T  P  E  R  L  P  Y  Q  E  A  V  Q  R  D  F  R  P  A  Q  V  G  D  S  F
 219 CGGACCCACATGGTGGACCTGCTGGTTCCGGGTGGAGCTGACCATCCCAGAGGCATGGGTGGGCCAGGAAGTTCACCTTTGCTGGGAAAGTGATGGAGAAGGTCTGGTG
  73 G  P  T  W  W  T  C  W  F  R  V  E  L  T  I  P  E  A  W  V  G  Q  E  V  H  L  C  W  E  S  D  G  E  G  L  V
 328 TGGCGTGATGGAGAACCTGTCCAGGGTTAACCAAAGAGGGTGAGAAGACCAGCTATGTCCTGACTGACAGGCTGGGGGAAAGAGACCCCCGAAGCCTCACTCTCTATG
 110 W  R  D  G  E  P  V  Q  G  L  T  K  E  G  E  K  T  S  Y  V  L  T  D  R  L  G  E  R  D  P  R  S  L  T  L  Y
 437 TGGAAGTAGCCTGCAATGGGCTCCTGGGGGCCGGGAAGGGAAGCATGATTGCAGCCCCTGACCCTGAGAAGATATTCCAGCTGAGCCGGGCTGAGCTAGCTGTGTTCCA
 146 V  E  V  A  C  N  G  L  L  G  A  G  K  G  S  M  I  A  A  P  D  P  E  K  I  F  Q  L  S  R  A  E  L  A  V  F  H
 546 CCGGGATGTCCACATGCTCCTGGTGGATCTGGAGCTGCTGCTGGGCATAGCCAAGGGCCTCGGGAAGGACAACCAGCGCAGCTTCCAGGCCCTGTACACAGCCAATCAG
 182 R  D  V  H  M  L  L  V  D  L  E  L  L  L  G  I  A  K  G  L  G  K  D  N  Q  R  S  F  Q  A  L  Y  T  A  N  Q
 655 ATGGTGAACGTGTGTGACCCTGCCCAGCCCGAGACCTTCCCAGTGGCCCAGGCCCTGGCCTCCAGGTTCTTTGGCCAACATGGGGGTGAAAGCCAACACACCATTCATG
 219 M  V  N  V  C  D  P  A  Q  P  E  T  F  P  V  A  Q  A  L  A  S  R  F  F  G  Q  H  G  G  E  S  Q  H  T  I  H
 764 CCACAGGGCACTGCCACATTGATACAGCCTGGCTTTGGCCCTTCAAAGAGACTGTGAGGAAATGTGCCCGGAGCTGGGTGACCGCCCTGCAGCTCATGGAGCGGAACCC
 255 A  T  G  H  C  H  I  D  T  A  W  L  W  P  F  K  E  T  V  R  K  C  A  R  S  W  V  T  A  L  Q  L  M  E  R  N  P
 873 TGAGTTCATCTTTGCCTGCTCCCAGGCGCAGCAGCTGGAATGGGTGAAGAGCCGCTACCCTGGCCTGTACTCCCGCATCCAGGAGTTTGCGTGCCGTGGGCAGTTTGTG
 291 E  F  I  F  A  C  S  Q  A  Q  Q  L  E  W  V  K  S  R  Y  P  G  L  Y  S  R  I  Q  E  F  A  C  R  G  Q  F  V
 982 CCTGTGGGGGGCACCTGGGTGGAAATGGATGGGAACCTGCCCAGTGGAGAGGCCATGGTGAGGCAGTTTTTGCAGGGCCAGAACTTCTTTCTGCAGGAGTTTGGGAAGA
 328 P  V  G  G  T  W  V  E  M  D  G  N  L  P  S  G  E  A  M  V  R  Q  F  L  Q  G  Q  N  F  F  L  Q  E  F  G  K
1091 TGTGCTCTGAGTTCTGGCTGCCGGACACCTTTGGCTACTCAGCACAGCTCCCCCAGATCATGCACGGCTGTGGCATCAGGCGCTTTCTCACCCAGAAATTGAGCTGGAA
 364 M  C  S  E  F  W  L  P  D  T  F  G  Y  S  A  Q  L  P  Q  I  M  H  G  C  G  I  R  R  F  L  T  Q  K  L  S  W  N
1200 TTTGGTGAACTCCTTCCCACACCATACATTTTTCTGGGAGGGCCTGGATGGCTCCCGTGTACTGGTCCACTTCCCACCTGGCGACTCCTATGGGATGCAGGGCAGCGTG
 400 L  V  N  S  F  P  H  H  T  F  F  W  E  G  L  D  G  S  R  V  L  V  H  F  P  P  G  D  S  Y  G  M  Q  G  S  V
1309 GAGGAGGTGCTGAAGACCGTGGCCAACAACCGGGACAAGGGGCGGGCCAACCACAGTGCCTTCCTCTTTGGCTTTGGGGATGGGGGTGGTGGCCCCACCCAGACCATGC
 437 E  E  V  L  K  T  V  A  N  N  R  D  K  G  R  A  N  H  S  A  F  L  F  G  F  G  D  G  G  G  G  P  T  Q  T  M
1418 TGGACCGCCTGAAGCGCCTGAGCAATACGGATGGGCTGCCCAGGGTGCAGCTATCTTCTCCAAGACAGCTCTTCTCAGCACTGGAGAGTGACTCAGAGCAGCTGTGCAC
 473 L  D  R  L  K  R  L  S  N  T  D  G  L  P  R  V  Q  L  S  S  P  R  Q  L  F  S  A  L  E  S  D  S  E  Q  L  C  T
1527 GTGGGTTGGGGAGCTCTTCTTGGAGCTGCACAATGGCACATACACCACCCATGCCCAGATCAAGAAGGGGAACCGGGAATGTGAGCGGATCCTGCACGACGTGGAGCTG
 509 W  V  G  E  L  F  L  E  L  H  N  G  T  Y  T  T  H  A  Q  I  K  K  G  N  R  E  C  E  R  I  L  H  D  V  E  L
1636 CTCAGTAGCCTGGCCCTGGCCCGCAGTGCCCAGTTCCTATACCCAGCAGCCCAGCTGCAGCACCTCTGGAGGCTCCTTCTTCTGAACCAGTTCCATGATGTGGTGACTG
 546 L  S  S  L  A  L  A  R  S  A  Q  F  L  Y  P  A  A  Q  L  Q  H  L  W  R  L  L  L  L  N  Q  F  H  D  V  V  T
1745 GAAGCTGCATCCAGATGGTGGCAGAGGAAGCCATGTGCCATTATGAAGACATCCGTTCCCATGGCAATACACTGCTCAGCGCTGCAGCCGCAGCCCTGTGTGCTGGGGA
 582 G  S  C  I  Q  M  V  A  E  E  A  M  C  H  Y  E  D  I  R  S  H  G  N  T  L  L  S  A  A  A  A  A  L  C  A  G  E
1854 GCCAGGTCCTGAGGGCCTCCTCATCGTCAACACACTGCCCTGGAAGCGGATCGAAGTGATGGCCCTGCCCAAACCGGGCGGGGCCCACAGCCTAGCCCTGGTGACAGTG
 618 P  G  P  E  G  L  L  I  V  N  T  L  P  W  K  R  I  E  V  M  A  L  P  K  P  G  G  A  H  S  L  A  L  V  T  V
1963 CCCAGCATGGGCTATGCTCCTGTTCCTCCCCCCACCTCACTGCAGCCCCTGCTGCCCCAGCAGCCTGTGTTCGTAGTGCAAGAGACTGATGGCTCCGTGACTCTGGACA
 655 P  S  M  G  Y  A  P  V  P  P  P  T  S  L  Q  P  L  L  P  Q  Q  P  V  F  V  V  Q  E  T  D  G  S  V  T  L  D
2072 ATGGCATCATCCGAGTGAAGCTGGACCCAACTGGTCGCCTGACGTCCTTGGTCCTGGTGGCCTCTGGCAGGGAGGCCATTGCTGAGGGCGCCGTGGGGAACCAGTTTGT
 691 N  G  I  I  R  V  K  L  D  P  T  G  R  L  T  S  L  V  L  V  A  S  G  R  E  A  I  A  E  G  A  V  G  N  Q  F  V
2181 GCTATTTGATGATGTCCCCTTGTACTGGGATGCATGGGACGTCATGGACTACCACCTGGAGACACGGAAGCCTGTGCTGGGCCAGGCAGGGACCCTGGCAGTGGGCACC
 727 L  F  D  D  V  P  L  Y  W  D  A  W  D  V  M  D  Y  H  L  E  T  R  K  P  V  L  G  Q  A  G  T  L  A  V  G  T
2290 GAGGGCGGCCTGCGGGGCAGCGCCTGGTTCTTGCTACAGATCAGCCCCAACAGTCGGCTTAGCCAGGAGGTTGTGCTGGACGTTGGCTGCCCCTATGTCCGCTTCCACA
 764 E  G  G  L  R  G  S  A  W  F  L  L  Q  I  S  P  N  S  R  L  S  Q  E  V  V  L  D  V  G  C  P  Y  V  R  F  H
2399 CCGAGGTACACTGGCATGAGGCCCACAAGTTCCTGAAGGTGGAGTTCCCTGCTCGCGTGCGGAGTTCCCAGGCCACCTATGAGATCCAGTTTGGGCACCTGCAGCGACC
 800 T  E  V  H  W  H  E  A  H  K  F  L  K  V  E  F  P  A  R  V  R  S  S  Q  A  T  Y  E  I  Q  F  G  H  L  Q  R  P
2508 TACCCACTACAATACCTCTTGGGACTGGGCTCGATTTGAGGTGTGGGCCCATCGCTGGATGGATCTGTCAGAACACGGCTTTGGGCTGGCCCTGCTCAACGACTGCAAG
 836 T  H  Y  N  T  S  W  D  W  A  R  F  E  V  W  A  H  R  W  M  D  L  S  E  H  G  F  G  L  A  L  L  N  D  C  K
2617 TATGGCGCGTCAGTGCGAGGCAGCATCCTCAGCCTCTCGCTCTTGCGGGCGCCTAAAGCCCCGGACGCTACTGCTGACACGGGGCGCCACGAGTTCACCTATGCACTGA
 873 Y  G  A  S  V  R  G  S  I  L  S  L  S  L  L  R  A  P  K  A  P  D  A  T  A  D  T  G  R  H  E  F  T  Y  A  L
2726 TGCCGCACAAGGGCTCTTTCCAGGATGCTGGCGTTATCCAAGCTGCCTACAGCCTAAACTTCCCCCTGTTGGCTCTGCCAGCCCCCAGCCCAGCGCCCGCCACCTCCTG
 909 M  P  H  K  G  S  F  Q  D  A  G  V  I  Q  A  A  Y  S  L  N  F  P  L  L  A  L  P  A  P  S  P  A  P  A  T  S  W
2835 GAGTGCGTTTTCCGTGTCTTCACCCGCGGTCGTATTGGAGACCGTCAAGCAGGCGGAGAGCAGCCCCCAGCGCCGCTCGCTGGTCCTGAGGCTGTATGAGGCCCACGGC
 945 S  A  F  S  V  S  S  P  A  V  V  L  E  T  V  K  Q  A  E  S  S  P  Q  R  R  S  L  V  L  R  L  Y  E  A  H  G
2944 AGCCACGTGGACTGCTGGCTGCACTTGTCGCTGCCGGTTCAGGAGGCCATCCTCTGCGATCTCTTGGAGCGACCAGACCCTGCTGGCCACTTGACTTCGGGACAACCGC
 982 S  H  V  D  C  W  L  H  L  S  L  P  V  Q  E  A  I  L  C  D  L  L  E  R  P  D  P  A  G  H  L  T  S  G  Q  P
3053 CTGAAGCTCACCTTTTCTCCCTTCCAAGTGCTGTCCCTGTTGCTCGTGCTTCAGCCTCCGCCACACTGAGTCCCTGGGGCTGGGGTTTTGTTTGTAGAAGGCTCTGGGG
1018 P  E  A  H  L  F  S  L  P  S  A  V  P  V  A  R  A  S  A  S  A  T  L  S  P  W  G  W  G  F  V  C  R  R  L  W  G
3162 ACTCCTAATTTCTGCTTCCCCAGCCTAA
1054 L  L  I  S  A  S  P  A
```

Figure 36A

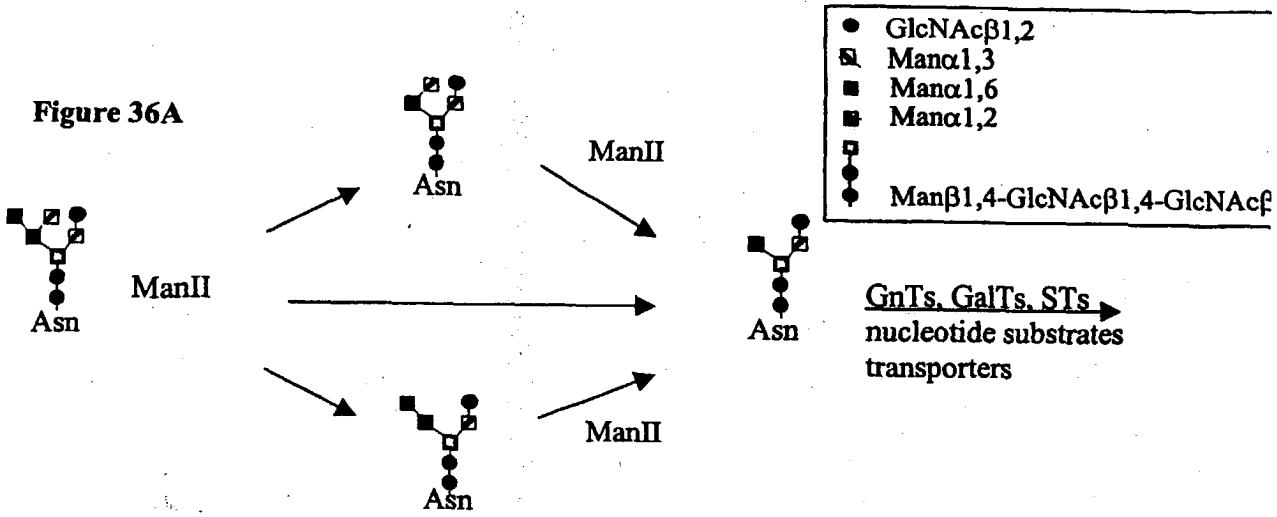

Figure 36B

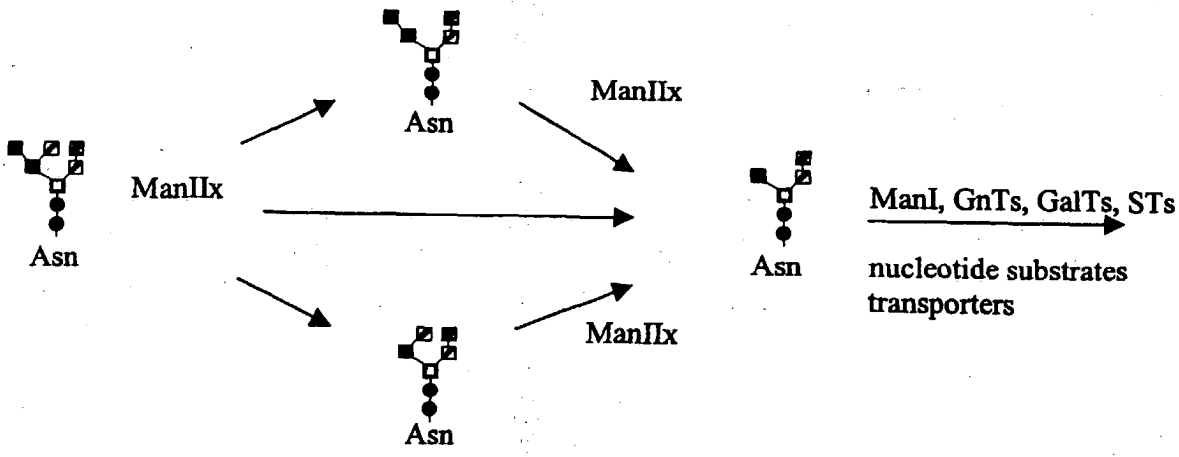
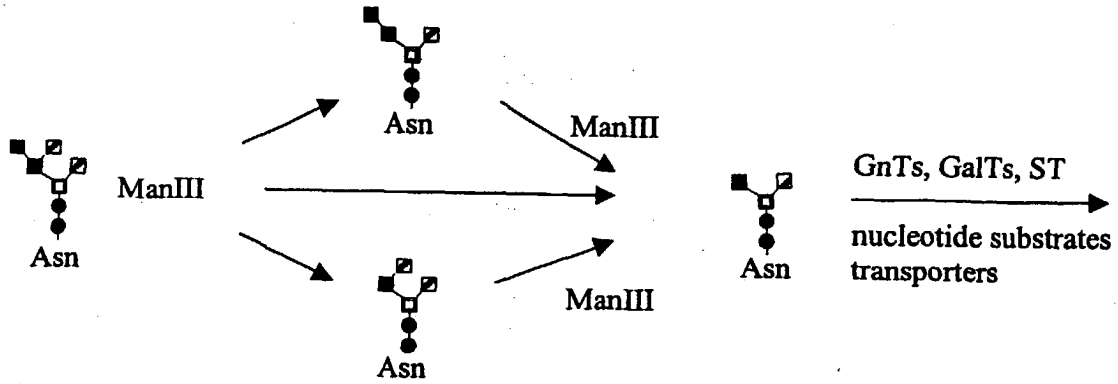
Figure 36C